



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 153815

TO: James Ketter
Location: REM/2A71/2C70
Art Unit: 1636
Friday, July 15, 2005
Case Serial Number: 10/804120

From: Toby Port
Location: Biotech-Chem Library
REM-1A59
Phone: 571-272-2523
toby.port@uspto.gov

Search Notes

Examiner Ketter,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Toby Port
X22523

This Page Blank (uspto)

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OM nucleic - nucleic search, using SW model

Run on: July 13, 2005, 17:30:50 ; Search time 82.6156 Seconds
(without alignments)
6003.565 Million cell updates/sec

Title: US-10-804-120-5

Perfect score: 79
Sequence: 1 gtaggttttttcgsggggtc.....ctatgacacaggttcaaca 79

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 6330947 seqs, 3139163630 residues

Total number of hits satisfying chosen parameters: 12661894

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications NA.*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
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10: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
11: /cgn2_6/ptodata/1/pubpna/US09C_NEW_PUB.seq.*
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18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq.*
19: /cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq.*
20: /cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq.*
21: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq.*
22: /cgn2_6/ptodata/1/pubpna/US10J_PUBCOMB.seq.*
23: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq.*
24: /cgn2_6/ptodata/1/pubpna/US11A_NEW_PUB.seq.*
25: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	79	100.0	79	9	US-09-810-521-5
2	79	100.0	79	9	US-09-801-321A-5
3	79	100.0	79	16	US-10-337-985-5
4	79	100.0	79	21	US-10-804-120-5
5	77.4	98.0	79	9	US-09-810-521-4
6	77.4	98.0	79	9	US-09-801-321A-4
7	77.4	98.0	79	16	US-10-337-985-4

Result No.	Score	Query Match	Length DB	ID	Description
8	77.4	98.0	79	21	US-10-804-120-4
9	77.4	98.0	1026	10	US-09-746-660A-53
10	77.4	98.0	1411	8	US-08-952-976-14
11	77.4	98.0	1411	14	US-10-226-136-14
12	77.4	98.0	3309400	9	US-09-738-626-1
13	61.6	78.0	80	9	US-09-810-521-6
14	61.6	78.0	80	9	US-09-801-321A-6
15	61.6	78.0	80	16	US-10-337-985-6
16	61.6	78.0	80	21	US-10-804-120-6
17	40	50.6	40	9	US-09-810-521-16
18	40	50.6	40	9	US-09-801-321A-14
19	40	50.6	40	16	US-10-337-985-14
20	40	50.6	40	21	US-10-804-120-14
21	33.6	42.5	40	9	US-09-810-521-18
22	33.6	42.5	40	9	US-09-801-321A-16
23	33.6	42.5	40	16	US-10-337-985-16
24	33.6	42.5	40	21	US-10-804-120-16
25	32.6	41.3	39	9	US-09-810-521-17
26	32.6	41.3	39	9	US-09-801-321A-15
27	32.6	41.3	39	16	US-10-337-985-15
28	32.6	41.3	39	21	US-10-804-120-15
29	28.4	35.7	30	14	US-10-067-974-25
30	28.2	35.7	47115	18	US-10-052-482-133
31	28	35.4	742	13	US-10-027-632-99671
32	28	35.4	742	13	US-10-027-632-99672
33	28	35.4	742	17	US-10-027-632-99671
34	28	35.4	742	17	US-10-027-632-99672
35	27.6	34.9	677	13	US-10-027-632-260979
36	27.6	34.9	677	17	US-10-027-632-260979
37	27.6	34.7	320	20	US-10-357-930-61115
38	27.2	34.4	36	9	US-09-810-521-15
39	27.2	34.4	36	9	US-09-801-321A-13
40	27.2	34.4	36	16	US-10-337-985-13
41	27.2	34.4	36	21	US-10-804-120-13
42	26.8	33.9	1007	13	US-10-027-632-252059
43	26.8	33.9	1007	17	US-10-027-632-252059
44	26.6	33.7	1071	18	US-10-335-977-2419
45	26.6	33.7	1248	18	US-10-335-977-2420

ALIGNMENTS

RESULT 1
US-09-810-521-5
Sequence 5, Appli
Patent No. US2002005153A1
GENERAL INFORMATION:
APPLICANT: KREUTZER, CAROLINE
APPLICANT: MOCKEL, BETTINA
APPLICANT: PEEPERLE, WALTER
APPLICANT: EGGELING, LOTMAR
APPLICANT: SAHM, HERMANN
TITLE OF INVENTION: L-LYSINE PRODUCING CORYNEBACTERIA AND
FILE REFERENCE: 21123/278416/MAS
CURRENT APPLICATION NUMBER: US/09/810,521
PRIOR FILING DATE: 2001-03-19
PRIOR APPLICATION NUMBER: DE 199 3114.8
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
LENGTH: 79
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: dapa promoter of C. glutamicum with the
NAME/KEY: mutation
LOCATION: (45)

US-09-810-521-5

Query Match 100.0%; Score 79; DB 9; Length 79;
Best Local Similarity 100.0%; Pred. No. 6e-19;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTAGGTTTTTGGGGGTTTAAACCCCAATGAGGGAAGTGTAACTTGAATC 60
Db 1 GTTAGGTTTTTGGGGGTTTAAACCCCAATGAGGGAAGTGTAACTTGAATC 60

Qy 61 TATGACACAGGTTTAA 79
Db 61 TATGACACAGGTTTAA 79

RESULT 2

US-09-801-321A-5
; Sequence 5, Application US/09801321A
; Publication No. US20020086371A1
; GENERAL INFORMATION:

; APPLICANT: Kreutzer, Caroline
; APPLICANT: Hans, Stephan
; APPLICANT: Rieping, Mechthild
; APPLICANT: Mockel, Bettina
; APPLICANT: Pfeifferle, Walter
; APPLICANT: Eggeling, Lothar
; APPLICANT: Sahn, Hermann
; APPLICANT: Patek, Mirosław
; TITLE OF INVENTION: L-Lysine-Producing Corynebacterium and Process for the Preparation
; FILE REFERENCE: 21123/278409
; CURRENT APPLICATION NUMBER: US/09/801.321A
; CURRENT FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 79
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(79)
; OTHER INFORMATION: dapA promoter of C. glutamicum carrying the MC20 mutation
; NAME/KEY: mutation
; LOCATION: (45)
US-09-801-321A-5

Query Match 100.0%; Score 79; DB 9; Length 79;
Best Local Similarity 100.0%; Pred. No. 6e-19;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTAGGTTTTTGGGGGTTTAAACCCCAATGAGGGAAGTGTAACTTGAATC 60
Db 1 GTTAGGTTTTTGGGGGTTTAAACCCCAATGAGGGAAGTGTAACTTGAATC 60

Qy 61 TATGACACAGGTTTAA 79
Db 61 TATGACACAGGTTTAA 79

RESULT 3

US-10-337-985-5
; Sequence 5, Application US/10337985
; Publication No. US20030162269A1
; GENERAL INFORMATION:

; APPLICANT: Kreutzer, Caroline
; APPLICANT: Hans, Stephan
; APPLICANT: Rieping, Mechthild
; APPLICANT: Mockel, Bettina
; APPLICANT: Pfeifferle, Walter
; APPLICANT: Eggeling, Lothar
; APPLICANT: Sahn, Hermann
; APPLICANT: Patek, Mirosław

; TITLE OF INVENTION: L-Lysine-Producing Corynebacterium and Process for the Preparation
; FILE REFERENCE: 21123/278409
; CURRENT APPLICATION NUMBER: US/10/337.985
; CURRENT FILING DATE: 2003-01-08
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 79
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(79)
; OTHER INFORMATION: dapA promoter of C. glutamicum carrying the MC20 mutation
; NAME/KEY: mutation
; LOCATION: (45)
US-10-337-985-5

Query Match 100.0%; Score 79; DB 16; Length 79;
Best Local Similarity 100.0%; Pred. No. 6e-19;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTAGGTTTTTGGGGGTTTAAACCCCAATGAGGGAAGTGTAACTTGAATC 60
Db 1 GTTAGGTTTTTGGGGGTTTAAACCCCAATGAGGGAAGTGTAACTTGAATC 60

Qy 61 TATGACACAGGTTTAA 79
Db 61 TATGACACAGGTTTAA 79

RESULT 4

US-10-804-120-5
; Sequence 5, Application US/10804120
; Publication No. US20050074791A1
; GENERAL INFORMATION:

; APPLICANT: Kreutzer, Caroline
; APPLICANT: Hans, Stephan
; APPLICANT: Rieping, Mechthild
; APPLICANT: Mockel, Bettina
; APPLICANT: Pfeifferle, Walter
; APPLICANT: Eggeling, Lothar
; APPLICANT: Sahn, Hermann
; APPLICANT: Patek, Mirosław
; TITLE OF INVENTION: L-Lysine-Producing Corynebacterium and Process for the Preparation
; FILE REFERENCE: 21123/278409
; CURRENT APPLICATION NUMBER: US/10/804.120
; CURRENT FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: US/10/337.985
; PRIOR FILING DATE: 2003-01-08
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 79
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(79)
; OTHER INFORMATION: dapA promoter of C. glutamicum carrying the MC20 mutation
; NAME/KEY: mutation
; LOCATION: (45)
US-10-804-120-5

Query Match 100.0%; Score 79; DB 21; Length 79;
Best Local Similarity 100.0%; Pred. No. 6e-19;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTAGGTTTTTGGGGGTTTAAACCCCAATGAGGGAAGTGTAACTTGAATC 60

Db 1 GTTAGGTTTTTGGCGGGGTGTTTAAACCCCAATGAGGAAGATGTAACCTTGAATC 60
Qy 61 TATGAGCACAGGTTTACA 79
Db 61 TATGAGCACAGGTTTACA 79

RESULT 5

US-09-810-521-4
; Sequence 4, Application US/09810521
; Patent No. US20020055153A1
; GENERAL INFORMATION:
; APPLICANT: KREUTZER, CAROLINE
; APPLICANT: MOCKEL, BETTINA
; APPLICANT: PFEFFERLE, WALTER
; APPLICANT: EGGELE, LOTMAR
; APPLICANT: SAHM, HERMANN
; APPLICANT: PATEK, MIROSLAV
; TITLE OF INVENTION: L-LYSINE PRODUCING CORYNEBACTERIA AND
; FILE REFERENCE: 21123/27846/MAS
; CURRENT APPLICATION NUMBER: US/09/810,521
; PRIOR FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: DE 199 31314.8
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 79
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; OTHER INFORMATION: dapa wild-type promoter
US-09-810-521-4

Query Match 98.0%; Score 77.4; DB 9; Length 79;
Best Local Similarity 98.7%; Pred. No. 2.3e-18;
Matches 78; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTAGGTTTTTGGCGGGGTGTTTAAACCCCAATGAGGAAGATGTAACCTTGAATC 60
Db 1 GTTAGGTTTTTGGCGGGGTGTTTAAACCCCAATGAGGAAGATGTAACCTTGAATC 60
Qy 61 TATGAGCACAGGTTTACA 79
Db 61 TATGAGCACAGGTTTACA 79

RESULT 6

US-09-801-321A-4
; Sequence 4, Application US/09801321A
; Publication No. US20020086371A1
; GENERAL INFORMATION:
; APPLICANT: KREUTZER, CAROLINE
; APPLICANT: HANS, STEPHAN
; APPLICANT: RIEPING, MECHTHILD
; APPLICANT: MOCKEL, BETTINA
; APPLICANT: PFEFFERLE, WALTER
; APPLICANT: SAHM, HERMANN
; APPLICANT: PATEK, MIROSLAV
; TITLE OF INVENTION: L-LYSINE-PRODUCING CORYNEBACTERIUM AND PROCESS FOR THE PREPARATIO
; FILE REFERENCE: 21123/278409
; CURRENT APPLICATION NUMBER: US/09/801,321A
; CURRENT FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 79
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum

; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(79)
; OTHER INFORMATION: dapa wild type promoter
US-09-801-321A-4

Query Match 98.0%; Score 77.4; DB 9; Length 79;
Best Local Similarity 98.7%; Pred. No. 2.3e-18;
Matches 78; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTAGGTTTTTGGCGGGGTGTTTAAACCCCAATGAGGAAGATGTAACCTTGAATC 60
Db 1 GTTAGGTTTTTGGCGGGGTGTTTAAACCCCAATGAGGAAGATGTAACCTTGAATC 60
Qy 61 TATGAGCACAGGTTTACA 79
Db 61 TATGAGCACAGGTTTACA 79

RESULT 7

US-10-337-985-4
; Sequence 4, Application US/10337985
; Publication No. US20030162269A1
; GENERAL INFORMATION:
; APPLICANT: KREUTZER, CAROLINE
; APPLICANT: HANS, STEPHAN
; APPLICANT: RIEPING, MECHTHILD
; APPLICANT: MOCKEL, BETTINA
; APPLICANT: PFEFFERLE, WALTER
; APPLICANT: EGGELE, LOTMAR
; APPLICANT: SAHM, HERMANN
; APPLICANT: PATEK, MIROSLAV
; TITLE OF INVENTION: L-LYSINE-PRODUCING CORYNEBACTERIUM AND PROCESS FOR THE PREPARATIO
; FILE REFERENCE: 21123/278409
; CURRENT APPLICATION NUMBER: US/10/337,985
; CURRENT FILING DATE: 2003-01-08
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 79
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(79)
; OTHER INFORMATION: dapa wild type promoter
US-10-337-985-4

Query Match 98.0%; Score 77.4; DB 16; Length 79;
Best Local Similarity 98.7%; Pred. No. 2.3e-18;
Matches 78; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTAGGTTTTTGGCGGGGTGTTTAAACCCCAATGAGGAAGATGTAACCTTGAATC 60
Db 1 GTTAGGTTTTTGGCGGGGTGTTTAAACCCCAATGAGGAAGATGTAACCTTGAATC 60
Qy 61 TATGAGCACAGGTTTACA 79
Db 61 TATGAGCACAGGTTTACA 79

RESULT 8

US-10-804-120-4
; Sequence 4, Application US/10804120
; Publication No. US20050074791A1
; GENERAL INFORMATION:
; APPLICANT: KREUTZER, CAROLINE
; APPLICANT: HANS, STEPHAN
; APPLICANT: RIEPING, MECHTHILD
; APPLICANT: MOCKEL, BETTINA
; APPLICANT: PFEFFERLE, WALTER
; APPLICANT: EGGELE, LOTMAR

APPLICANT: Sahn, Hermann
APPLICANT: Patek, Miroslav
TITLE OF INVENTION: L-Lysine-Producing Corynebacterium and Process for the Preparation
FILE REFERENCE: 21123/278409
CURRENT APPLICATION NUMBER: US/10/804,120
CURRENT FILING DATE: 2004-03-19
PRIOR APPLICATION NUMBER: US/10/337,985
PRIOR FILING DATE: 2003-01-08
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4
LENGTH: 79
TYPE: DNA
ORGANISM: Corynebacterium glutamicum
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)..(79)
OTHER INFORMATION: dapa wild type promoter
US-10-804-120-4

Query Match 98.0%; Score 77.4; DB 21; Length 79;
Best Local Similarity 98.7%; Pred. No. 2.3e-18;
Matches 78; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTAGGTTTTTGGGGGTTTAAACCCCAATGAGGAGATGTAACCTTGAATC 60
Db 1 GTTAGGTTTTTGGGGGTTTAAACCCCAATGAGGAGATGTAACCTTGAATC 60
Qy 61 TATGACACAGGTTTAA 79
Db 61 TATGACACAGGTTTAA 79

RESULT 9
US-09-746-660A-53
Sequence 53, Application US/09746660A
Publication No. US20030049804A1
GENERAL INFORMATION:
APPLICANT: Pompejus, Markus
APPLICANT: Krogger, Burkhard
APPLICANT: Schroder, Hartwig
APPLICANT: Zelder, Oskar
APPLICANT: Haberhauer, Gregor
APPLICANT: Kim, Jun-Won
APPLICANT: Lee, Heung-Schick
APPLICANT: Hwang, Byung-Joon
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
FILE REFERENCE: BGI-121C22
CURRENT APPLICATION NUMBER: US/09/746,660A
CURRENT FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 09/606740
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: 09/603124
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: 60/141031
PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: 60/142101
PRIOR FILING DATE: 1999-07-02
PRIOR APPLICATION NUMBER: 60/148613
PRIOR FILING DATE: 1999-08-12
PRIOR APPLICATION NUMBER: 60/187970
PRIOR FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: DE 19931420.9
PRIOR FILING DATE: 1999-07-08
NUMBER OF SEQ ID NOS: 125
SOFTWARE: PatentIn Vers. 2.0
SEQ ID NO 53
LENGTH: 1026
TYPE: DNA
ORGANISM: Corynebacterium glutamicum
FEATURE:

NAME/KEY: CDS
LOCATION: (101)..(1003)
OTHER INFORMATION: RXA00865
US-09-746-660A-53

Query Match 98.0%; Score 77.4; DB 10; Length 1026;
Best Local Similarity 98.7%; Pred. No. 4.8e-18;
Matches 78; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTAGGTTTTTGGGGGTTTAAACCCCAATGAGGAGATGTAACCTTGAATC 60
Db 40 GTTAGGTTTTTGGGGGTTTAAACCCCAATGAGGAGATGTAACCTTGAATC 99
Qy 61 TATGACACAGGTTTAA 79
Db 100 TATGACACAGGTTTAA 118

RESULT 10
US-08-952-976-14

Sequence 14, Application US/08952976
Publication No. US20020086370A1
GENERAL INFORMATION:

APPLICANT: OTSUNA, Seiko
APPLICANT: SUGIMOTO, Masakazu
APPLICANT: IZUI, Masako
APPLICANT: HAYAKAWA, Atsushi
APPLICANT: NAKANO, Bichi
APPLICANT: KOBAYASHI, Masaki
APPLICANT: YOSHIMURA, Yasuhiko
APPLICANT: NAKAMATSU, Tsuyoshi
TITLE OF INVENTION: METHOD OF PRODUCING L-LYSINE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MATER & NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/952,976
FILING DATE: 8-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-140614
FILING DATE: 07-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: NORMAN F. OBLON
REGISTRATION NUMBER: 24,618
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 1411 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Brevibacterium lactofermentum
STRAIN: ATCC 13869
FEATURE:
NAME/KEY: CDS
LOCATION: 311..1213
US-08-952-976-14

Query Match 98.0%; Score 77.4; DB 8; Length 1411;
Best Local Similarity 98.7%; Pred. No. 5.2e-18;
Matches 78; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTAGGTTTTTGGGGGTTGTTTAAACCCCAATGAGGGAAGATGTACCTTGAATC 60
DB 250 GTTAGGTTTTTGGGGGTTGTTTAAACCCCAATGAGGGAAGATGTACCTTGAATC 309
QY 61 TATGACACAGGTTTACA 79
DB 310 TATGACACAGGTTTACA 328

RESULT 11

US-10-226-136-14
Sequence 14, Application US/10226136
Publication No. US2003054506A1
GENERAL INFORMATION:

APPLICANT: OTSUNA, Seiko
SUGIMOTO, Masakazu
IZUI, Masako
HAYAKAWA, Atsuehi
NAKANO, Eiichi
KOBAYASHI, Masaki
YOSHIMURA, Yasuhiko
NAKAMATSU, Tsuyoshi

TITLE OF INVENTION: METHOD OF PRODUCING L-LYSINE

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VA

COUNTRY: USA
ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 23-Aug-2002
APPLICATION NUMBER: US/10/226,136
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/952,976
FILING DATE: 8-DEC-1997
APPLICATION NUMBER: JP 7-140614
FILING DATE: 07-JUL-1995

ATTORNEY/AGENT INFORMATION:
NAME: NORMAN F. OBLON
REGISTRATION NUMBER: 24,618
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220

INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:

LENGTH: 1411 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Brevibacterium lactofermentum
STRAIN: ATCC 13869

FEATURE:
NAME/KEY: CDS
LOCATION: 311..1213

SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-226-136-14

Query Match 98.0%; Score 77.4; DB 14; Length 1411;
Best Local Similarity 98.7%; Pred. No. 5.2e-18;
Matches 78; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTAGGTTTTTGGGGGTTGTTTAAACCCCAATGAGGGAAGATGTACCTTGAATC 60
DB 250 GTTAGGTTTTTGGGGGTTGTTTAAACCCCAATGAGGGAAGATGTACCTTGAATC 309
QY 61 TATGACACAGGTTTACA 79
DB 310 TATGACACAGGTTTACA 328

RESULT 12

US-09-738-626-1/c
Sequence 1, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:

APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: SENOH, AKIHRO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO

TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES

FILE REFERENCE: 249-125

CURRENT APPLICATION NUMBER: US/09/738,626

PRIOR FILING DATE: 2000-12-18

PRIOR APPLICATION NUMBER: JP 99/377484

PRIOR FILING DATE: 1999-12-16

PRIOR APPLICATION NUMBER: JP 00/159162

PRIOR FILING DATE: 2000-04-07

PRIOR APPLICATION NUMBER: JP 00/280988

PRIOR FILING DATE: 2000-08-03

NUMBER OF SEQ ID NOS: 7059

SOFTWARE: Patentin ver. 3.0

SEQ ID NO 1

LENGTH: 3309400

TYPE: DNA

ORGANISM: Corynebacterium glutamicum

US-09-738-626-1

Query Match 98.0%; Score 77.4; DB 9; Length 3309400;
Best Local Similarity 98.7%; Pred. No. 4.7e-17;
Matches 78; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTAGGTTTTTGGGGGTTGTTTAAACCCCAATGAGGGAAGATGTACCTTGAATC 60
DB 2080244 GTTAGGTTTTTGGGGGTTGTTTAAACCCCAATGAGGGAAGATGTACCTTGAATC 2080185
QY 61 TATGACACAGGTTTACA 79
DB 2080184 TATGACACAGGTTTACA 2080166

RESULT 13

US-09-810-521-6
Sequence 6, Application US/09810521
Patent No. US20020055153A1
GENERAL INFORMATION:

APPLICANT: KREUTZER, CAROLINE
APPLICANT: MOCKEL, BETTINA
APPLICANT: PFEFFERLE, WALTER
APPLICANT: EGGELE, LOTMAR
APPLICANT: SAHM, HERMANN
APPLICANT: PATEK, MIROSLAV

TITLE OF INVENTION: L-LYSINE PRODUCING CORNEBACTERIA AND
TITLE OF INVENTION: PROCESS FOR THE PREPARATION OF LYSINE
FILE REFERENCE: 21123/278416/MAS

```

; CURRENT APPLICATION NUMBER: US/09/810,521
; CURRENT FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: DE 199 31314.8
; PRIOR FILING DATE: 1999-05-07
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 80
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: dapa promoter of C. glutamicum with the
; NAME/KEY: mutation
; LOCATION: (35)..(53)
; US-09-810-521-6

Query Match          78.0%; Score 61.6; DB 9; Length 80;
Best Local Similarity 93.8%; Pred. No. 1.5e-12;
Matches 75; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 1 GTTAGGTTTTTGGGGGTTTAAACCC- AAATGAGGAAAGATGTAACCTTGAAC 59
    |||||
DB 1 GTTAGGTTTTTGGGGGTTTAAACCCCAAAATGAGGAAAGATGTAATTTGAAC 60
    |||||

QY 60 CTATGACACAGGTTTAA 79
    |||||
DB 61 CTATGACACAGGTTTAA 80
    |||||

RESULT 14
US-09-801-321A-6
; Sequence 6, Application US/09801321A
; Publication No. US20020086371A1
; GENERAL INFORMATION:
; APPLICANT: Kreutzer, Caroline
; APPLICANT: Hans, Stephan
; APPLICANT: Rieping, Mechthild
; APPLICANT: Mockel, Bettina
; APPLICANT: Pfeifferle, Walter
; APPLICANT: Eggeling, Lothar
; APPLICANT: Sahm, Hermann
; APPLICANT: Patek, Miroslav
; TITLE OF INVENTION: L-Lysine-Producing Corynebacterium and Process for the Preparation
; FILE REFERENCE: 21123/278409
; CURRENT APPLICATION NUMBER: US/09/801,321A
; CURRENT FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 80
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(80)
; OTHER INFORMATION: dapa promoter of C. glutamicum carrying the MA16 mutation
; NAME/KEY: mutation
; LOCATION: (35)..(53)
; US-09-801-321A-6

Query Match          78.0%; Score 61.6; DB 9; Length 80;
Best Local Similarity 93.8%; Pred. No. 1.5e-12;
Matches 75; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 1 GTTAGGTTTTTGGGGGTTTAAACCC- AAATGAGGAAAGATGTAACCTTGAAC 59
    |||||
DB 1 GTTAGGTTTTTGGGGGTTTAAACCCCAAAATGAGGAAAGATGTAATTTGAAC 60
    |||||

QY 60 CTATGACACAGGTTTAA 79
    |||||
DB 61 CTATGACACAGGTTTAA 80
    |||||

US-10-337-985-6
; Sequence 6, Application US/10337985
; Publication No. US20030162259A1
; GENERAL INFORMATION:
; APPLICANT: Kreutzer, Caroline
; APPLICANT: Hans, Stephan
; APPLICANT: Rieping, Mechthild
; APPLICANT: Mockel, Bettina
; APPLICANT: Pfeifferle, Walter
; APPLICANT: Eggeling, Lothar
; APPLICANT: Sahm, Hermann
; APPLICANT: Patek, Miroslav
; TITLE OF INVENTION: L-Lysine-Producing Corynebacterium and Process for the Preparation
; FILE REFERENCE: 21123/278409
; CURRENT APPLICATION NUMBER: US/10/337,985
; CURRENT FILING DATE: 2003-01-08
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 80
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(80)
; OTHER INFORMATION: dapa promoter of C. glutamicum carrying the MA16 mutation
; NAME/KEY: mutation
; LOCATION: (35)..(53)
; US-10-337-985-6

Query Match          78.0%; Score 61.6; DB 16; Length 80;
Best Local Similarity 93.8%; Pred. No. 1.5e-12;
Matches 75; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 1 GTTAGGTTTTTGGGGGTTTAAACCC- AAATGAGGAAAGATGTAACCTTGAAC 59
    |||||
DB 1 GTTAGGTTTTTGGGGGTTTAAACCCCAAAATGAGGAAAGATGTAATTTGAAC 60
    |||||

QY 60 CTATGACACAGGTTTAA 79
    |||||
DB 61 CTATGACACAGGTTTAA 80
    |||||

Search completed: July 13, 2005, 22:08:22
Job time : 86.6156 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OW nucleic - nucleic search, using sw model

Run on: July 13, 2005, 17:08:30 ; Search time 19.2529 Seconds
(without alignments)
6714.112 Million cell updates/sec

Title: US-10-804-120-5

Perfect score: 79

Sequence: 1 gtagagtttttgcgggggtt.....ctatgacacagtttaca 79

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /cgn2_6/prodata/1/ina/5A_COMB.seq:*
- 2: /cgn2_6/prodata/1/ina/5B_COMB.seq:*
- 3: /cgn2_6/prodata/1/ina/6A_COMB.seq:*
- 4: /cgn2_6/prodata/1/ina/6B_COMB.seq:*
- 5: /cgn2_6/prodata/1/ina/PCTUS_COMB.seq:*
- 6: /cgn2_6/prodata/1/ina/backfile01.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	79	100.0	79	3 US-09-353-133-5	Sequence 5, Appl1
2	79	100.0	79	4 US-10-337-985-5	Sequence 5, Appl1
3	77.4	98.0	79	3 US-09-353-133-4	Sequence 4, Appl1
4	77.4	98.0	79	4 US-10-337-985-4	Sequence 4, Appl1
5	77.4	98.0	1411	1 US-08-674-168-18	Sequence 18, Appl1
6	77.4	98.0	1411	3 US-08-985-908-14	Sequence 14, Appl1
7	77.4	98.0	1411	3 US-08-852-730-19	Sequence 19, Appl1
8	61.6	78.0	80	3 US-09-353-133-6	Sequence 6, Appl1
9	61.6	78.0	80	4 US-10-337-985-6	Sequence 6, Appl1
10	40	50.6	40	4 US-10-337-985-14	Sequence 14, Appl1
11	33.6	42.5	40	4 US-10-337-985-16	Sequence 16, Appl1
12	32.6	41.3	39	4 US-10-337-985-15	Sequence 15, Appl1
13	27.2	34.4	36	4 US-09-337-985-13	Sequence 13, Appl1
14	26.4	33.4	601	4 US-09-949-001-402	Sequence 402, App
15	26.4	33.4	312957	4 US-09-949-001-31	Sequence 31, Appl1
16	26.4	33.4	312972	4 US-09-949-001-34	Sequence 34, Appl1
17	26.2	33.2	32958	4 US-09-949-016-138753	Sequence 138753, A
18	25.8	32.7	32958	4 US-09-949-016-15677	Sequence 15677, A
19	25.8	32.7	36317	4 US-09-949-016-12697	Sequence 12697, A
20	25.8	32.7	36332	4 US-09-949-016-14047	Sequence 14047, A
21	25	31.6	601	4 US-09-949-016-138754	Sequence 138754, A
22	25	31.6	1431	1 US-08-451-715A-11	Sequence 11, Appl1
23	25	31.6	194889	4 US-09-949-016-15654	Sequence 15654, A
24	24.6	31.1	601	4 US-09-949-016-46647	Sequence 46647, A
25	24.6	31.1	14761	4 US-09-949-016-14181	Sequence 14181, A
26	24.6	31.1	14823	4 US-09-949-016-12124	Sequence 12124, A
27	24.6	31.1	89689	4 US-09-949-016-13089	Sequence 13089, A

C	28	24.4	30.9	601	4	US-09-949-016-45241	Sequence 45241, A
	29	24.4	30.9	18888	4	US-09-949-016-16386	Sequence 16386, A
	30	24.4	30.9	27223	4	US-09-949-016-11036	Sequence 11036, A
	31	24.2	30.6	601	4	US-09-949-016-113337	Sequence 113337, A
	32	24.2	30.6	705	4	US-09-107-532A-1629	Sequence 1629, Ap
	33	24.2	30.6	2142	4	US-09-949-016-4818	Sequence 4818, Ap
	34	24.2	30.6	2474	4	US-09-774-528-137	Sequence 137, App
	35	24.2	30.6	21045	4	US-09-949-016-16560	Sequence 16560, A
	36	24.2	30.6	155266	4	US-09-949-016-113870	Sequence 113870, A
	37	24.2	30.6	285986	4	US-09-949-016-13287	Sequence 13287, A
	38	24.2	30.6	288031	4	US-09-949-016-14864	Sequence 14864, A
	39	23.8	30.1	365	4	US-09-270-767-6267	Sequence 6267, Ap
	40	23.8	30.1	365	4	US-09-270-767-21549	Sequence 21549, A
	41	23.8	30.1	15817	4	US-09-949-016-16496	Sequence 16496, A
	42	23.6	29.9	654	3	US-08-936-165A-234	Sequence 234, App
	43	23.6	29.9	936	3	US-08-910-501-3	Sequence 3, Appl1
	44	23.6	29.9	936	3	US-09-398-550-3	Sequence 3, Appl1
	45	23.6	29.9	939	3	US-08-910-501-1	Sequence 1, Appl1

ALIGNMENTS

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RESULT 1
US-09-353-133-5
; Sequence 5, Application US/09353133
; Patent No. 6200785
; GENERAL INFORMATION:
; APPLICANT: Degussa-Höls AG
; APPLICANT: Forschungszentrum Jülich GmbH
; TITLE OF INVENTION: L-lysine-producing Corynebacteria and process for the
; TITLE OF INVENTION: L-lysine-producing Corynebacteria and process for the
; FILE REFERENCE: 990058 BT
; CURRENT APPLICATION NUMBER: US/09/353,133
; CURRENT FILING DATE: 1999-07-14
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 5
; LENGTH: 79
; TYPE: DNA
; ORGANISM: Synthetic sequence
; FEATURE:
; OTHER INFORMATION: Description of the synthetic sequence:
; OTHER INFORMATION: dapa promoter of C. glutamicum with the
; OTHER INFORMATION: MC20-Mutation
; FEATURE:
; NAME/KEY: mutation
; LOCATION: (45)
; US-09-353-133-5

Query Match          100.0%; Score 79; DB 3; Length 79;
Best Local Similarity 100.0%; Pred. No. 1.1e-21;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTAGGTTTTCGCGGGTTGTTTAAACCCCAATGAGGAAGATGTAACCTTGAATC 60
DB 1 GTTAGGTTTTCGCGGGTTGTTTAAACCCCAATGAGGAAGATGTAACCTTGAATC 60
DB 61 TATGACACAGGTTTAA 79
DB 61 TATGACACAGGTTTAA 79

RESULT 2
US-10-337-985-5
; Sequence 5, Application US/10337985
; Patent No. 6746855
; GENERAL INFORMATION:
; APPLICANT: Kreutzer, Caroline
; APPLICANT: Hans, Stephan
; APPLICANT: Rieping, Mechthild
; APPLICANT: Mockel, Bettina
; APPLICANT: Pfeifferle, Walter

```

```

; APPLICANT: Eggeling, Lothar
; APPLICANT: Sahm, Hermann
; APPLICANT: Patek, Miroslav
; TITLE OF INVENTION: L-Lysine-Producing Corynebacterium and Process for the Preparation
; TITLE OF INVENTION: of L-Lysine
; FILE REFERENCE: 21123/278409
; CURRENT APPLICATION NUMBER: US/10/337,985
; CURRENT FILING DATE: 2003-01-08
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 79
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(79)
; OTHER INFORMATION: dapa promoter of C. glutamicum carrying the MC20 mutation
; FEATURE:
; NAME/KEY: mutation
; LOCATION: (45)
; US-10-337-985-5
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Query Match          100.0%; Score 79; DB 4; Length 79;
Best Local Similarity 100.0%; Pred. No. 1.1e-21;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 GTTAGGTTTTTGGGGGTTGTTAAACCCCAATGAGGAGATGTTAAGTTGAATC 60
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DB 1 GTTAGGTTTTTGGGGGTTGTTAAACCCCAATGAGGAGATGTTAAGTTGAATC 60
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QY 61 TATGACACAGGTTTAA 79
    |||
DB 61 TATGACACAGGTTTAA 79
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RESULT 3
US-09-353-133-4
; Sequence 4, Application US/09353133
; Patent No. 6200785
; GENERAL INFORMATION:
; APPLICANT: Degussa-Höls AG
; TITLE OF INVENTION: L-Lysine-producing corynebacteria and process for the
; TITLE OF INVENTION: preparation of L-Lysine
; FILE REFERENCE: 990058 BT
; CURRENT APPLICATION NUMBER: US/09/353,133
; CURRENT FILING DATE: 1999-07-14
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 79
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; OTHER INFORMATION: dapa wild-type promoter
; US-09-353-133-4
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Query Match          98.0%; Score 77.4; DB 3; Length 79;
Best Local Similarity 98.7%; Pred. No. 4.8e-21;
Matches 78; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 1 GTTAGGTTTTTGGGGGTTGTTAAACCCCAATGAGGAGATGTTAAGTTGAATC 60
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DB 1 GTTAGGTTTTTGGGGGTTGTTAAACCCCAATGAGGAGATGTTAAGTTGAATC 60
    |||
QY 61 TATGACACAGGTTTAA 79
    |||
DB 61 TATGACACAGGTTTAA 79
    |||
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```

RESULT 4
US-10-337-985-4
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```

; Sequence 4, Application US/10337985
; Patent No. 6746855
; GENERAL INFORMATION:
; APPLICANT: Kreutzer, Caroline
; APPLICANT: Hans, Stephan
; APPLICANT: Rieping, Mechthild
; APPLICANT: Mockel, Bettina
; APPLICANT: Pfeifferle, Walter
; APPLICANT: Eggeling, Lothar
; APPLICANT: Sahm, Hermann
; TITLE OF INVENTION: L-Lysine-Producing Corynebacterium and Process for the Preparation
; TITLE OF INVENTION: of L-Lysine
; FILE REFERENCE: 21123/278409
; CURRENT APPLICATION NUMBER: US/10/337,985
; CURRENT FILING DATE: 2003-01-08
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 79
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(79)
; OTHER INFORMATION: dapa wild type promoter
; US-10-337-985-4
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Query Match          98.0%; Score 77.4; DB 4; Length 79;
Best Local Similarity 98.7%; Pred. No. 4.8e-21;
Matches 78; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 1 GTTAGGTTTTTGGGGGTTGTTAAACCCCAATGAGGAGATGTTAAGTTGAATC 60
    |||
DB 1 GTTAGGTTTTTGGGGGTTGTTAAACCCCAATGAGGAGATGTTAAGTTGAATC 60
    |||
QY 61 TATGACACAGGTTTAA 79
    |||
DB 61 TATGACACAGGTTTAA 79
    |||
```

```

RESULT 5
US-08-674-168-18
; Sequence 18, Application US/08674168
; Patent No. 5804414
; GENERAL INFORMATION:
; APPLICANT: MORIYA, Mika
; APPLICANT: MATSUI, Hiroshi
; APPLICANT: YOKOZAKI, Kenzo
; APPLICANT: HIRANO, Seiko
; APPLICANT: HAYAKAWA, Atsushi
; APPLICANT: IZUI, Masako
; APPLICANT: SUGIMOTO, Masakazu
; TITLE OF INVENTION: METHOD OF AMPLIFYING GENE USING
; TITLE OF INVENTION: ARTIFICIAL TRANSPOSON
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 JEFFERSON DAVIS HIGHWAY, SUITE # 400
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/674,168
; FILING DATE: 01-JUL-1996
; CLASSIFICATION: 435
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-166541
FILING DATE: 30-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-810-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 1411 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Brevibacterium lactofermentum
STRAIN: ATCC 13869
FEATURE:
NAME/KEY: CDS
LOCATION: 311..1213
US-08-674-168-18

Query Match 98.0%; Score 77.4; DB 1; Length 1411;
Best Local Similarity 98.7%; Pred. No. 1.5e-20;
Matches 78; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTAGGTTTTTGGCGGGTTGTTTAAACCCCAATGAGGGAAGATGTAACCTTGAACTC 60
Db 250 GTTAGGTTTTTGGCGGGTTGTTTAAACCCCAATGAGGGAAGATGTAACCTTGAACTC 309

Qy 61 TATGAGCACAGGTTTAA 79
Db 310 TATGAGCACAGGTTTAA 328

RESULT 6
US-08-985-908-14
Sequence 14, Application US/08985908
Patent No. 6004773
GENERAL INFORMATION:
APPLICANT: MASAYUKI ARAKI, MASAKAZU SUGIMOTO, YASUHIKO YOSHIMURA, AND TSUYOSHI NA
TITLE OF INVENTION: METHOD FOR PRODUCING L-LYSINE
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,908
FILING DATE: 05-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-325659
FILING DATE: 05-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: NORMAN F. OBLON
REGISTRATION NUMBER: 24,618
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:
LENGTH: 1411 bases
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
ORIGINAL SOURCE:
ORGANISM: Brevibacterium lactofermentum
STRAIN: ATCC 13869
FEATURE:
NAME/KEY: CDS
LOCATION: 311..1213
US-08-985-908-14

Query Match 98.0%; Score 77.4; DB 3; Length 1411;
Best Local Similarity 98.7%; Pred. No. 1.5e-20;
Matches 78; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTAGGTTTTTGGCGGGTTGTTTAAACCCCAATGAGGGAAGATGTAACCTTGAACTC 60
Db 250 GTTAGGTTTTTGGCGGGTTGTTTAAACCCCAATGAGGGAAGATGTAACCTTGAACTC 309

Qy 61 TATGAGCACAGGTTTAA 79
Db 310 TATGAGCACAGGTTTAA 328

RESULT 7
US-08-852-730-19
Sequence 19, Application US/08852730
Patent No. 6090597
GENERAL INFORMATION:
APPLICANT: SEIKO HIRANO, MASAKAZU SUGIMOTO, EIICHI NAKANO,
APPLICANT: MASAO IZUI, ATSUSHI HAYAKAWA, YASUHIKO YOSHIMURA, AND TSUYOSHI
APPLICANT: NAKAMATSU
TITLE OF INVENTION: METHOD OF PRODUCING L-LYSINE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER AND NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY
CITY: ARLINGTON
STATE: VA
ZIP: 22026
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/852,730
FILING DATE: 05-07-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-142812
FILING DATE: 05-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: NORMAN F. OBLON
REGISTRATION NUMBER: 24,618
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 1411 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
ORIGINAL SOURCE:
ORGANISM: Brevibacterium lactofermentum
STRAIN: ATCC 13869
FEATURE:
NAME/KEY: CDS

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LOCATION: 311..1213
US-08-852-730-19
Query Match      98.0%; Score 77.4; DB 3; Length 1411;
Best Local Similarity 98.7%; Pred. No. 1.5e-20;
Matches 78; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTAGGTTTTTGGGGGTTTAAACCCCAATGAGGAGATGTAACCTTGAATC 60
DB 250 GTTAGGTTTTTGGGGGTTTAAACCCCAATGAGGAGATGTAACCTTGAATC 309

QY 61 TATGAGCACAGGTTTAA 79
DB 310 TATGAGCACAGGTTTAA 328

RESULT 8
US-09-353-133-6
Sequence 6, Application US/09353133
Patent No. 6200785
GENERAL INFORMATION:
APPLICANT: Degussa-Hols AG
APPLICANT: Forschungszentrum Juelich GmbH
TITLE OF INVENTION: L-Lysine-producing corynebacteria and process for the
FILE REFERENCE: 990058 BT
CURRENT APPLICATION NUMBER: US/09/353,133
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
LENGTH: 80
TYPE: DNA
ORGANISM: Synthetic sequence
FEATURE:
OTHER INFORMATION: Description of the synthetic sequence:
OTHER INFORMATION: dapA promoter of C. glutamicum with the
FEATURE:
NAME/KEY: mutation
LOCATION: (35)..(53)
US-09-353-133-6

Query Match      78.0%; Score 61.6; DB 3; Length 80;
Best Local Similarity 93.8%; Pred. No. 8.6e-15;
Matches 75; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 1 GTTAGGTTTTTGGGGGTTTAAACCCCAATGAGGAGATGTAACCTTGAATC 59
DB 1 GTTAGGTTTTTGGGGGTTTAAACCCCAATGAGGAGATGTAACCTTGAATC 60

QY 60 CTATGAGCACAGGTTTAA 79
DB 61 CTATGAGCACAGGTTTAA 80

RESULT 9
US-10-337-985-6
Sequence 6, Application US/10337985
Patent No. 6746855
GENERAL INFORMATION:
APPLICANT: Kreutzler, Caroline
APPLICANT: Hans, Stephan
APPLICANT: Rieping, Mechthild
APPLICANT: Mockel, Bettina
APPLICANT: Pfeifferle, Walter
APPLICANT: Eggeling, Lothar
APPLICANT: Sahm, Hermann
APPLICANT: Patek, Mirosław
TITLE OF INVENTION: L-Lysine-Producing Corynebacterium and Process for the Preparatio
FILE REFERENCE: 21123/278409
FILE REFERENCE: 21123/278409
CURRENT APPLICATION NUMBER: US/10/337,985
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CURRENT FILING DATE: 2003-01-08
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin version 3.0
SEQ ID NO 6
LENGTH: 80
TYPE: DNA
ORGANISM: Artificial
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)..(80)
OTHER INFORMATION: dapA promoter of C. glutamicum carrying the MA16 mutation
FEATURE:
NAME/KEY: mutation
LOCATION: (35)..(53)
US-10-337-985-6

Query Match      78.0%; Score 61.6; DB 4; Length 80;
Best Local Similarity 93.8%; Pred. No. 8.6e-15;
Matches 75; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 1 GTTAGGTTTTTGGGGGTTTAAACCCCAATGAGGAGATGTAACCTTGAATC 59
DB 1 GTTAGGTTTTTGGGGGTTTAAACCCCAATGAGGAGATGTAACCTTGAATC 60

QY 60 CTATGAGCACAGGTTTAA 79
DB 61 CTATGAGCACAGGTTTAA 80

RESULT 10
US-10-337-985-14/C
Sequence 14, Application US/10337985
Patent No. 6746855
GENERAL INFORMATION:
APPLICANT: Kreutzler, Caroline
APPLICANT: Hans, Stephan
APPLICANT: Rieping, Mechthild
APPLICANT: Mockel, Bettina
APPLICANT: Pfeifferle, Walter
APPLICANT: Eggeling, Lothar
APPLICANT: Sahm, Hermann
APPLICANT: Patek, Mirosław
TITLE OF INVENTION: L-Lysine-Producing Corynebacterium and Process for the Preparatio
FILE REFERENCE: 21123/278409
CURRENT APPLICATION NUMBER: US/10/337,985
CURRENT FILING DATE: 2003-01-08
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin version 3.0
SEQ ID NO 14
LENGTH: 40
TYPE: DNA
ORGANISM: Artificial
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)..(40)
OTHER INFORMATION: PCR primer
US-10-337-985-14

Query Match      50.6%; Score 40; DB 4; Length 40;
Best Local Similarity 100.0%; Pred. No. 2.3e-06;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 CCAATGAGGAGATGTAACCTTGAATCTATGAGCAC 69
DB 40 CCAATGAGGAGATGTAACCTTGAATCTATGAGCAC 1

RESULT 11
US-10-337-985-16/C
Sequence 16, Application US/10337985
Patent No. 6746855
GENERAL INFORMATION:
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; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH OSTEOPOROSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1000789
; CURRENT APPLICATION NUMBER: US/09/949,001
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 60/231,323
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 848
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 312957
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(312957)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-001-31

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Query_Match      33.4%; Score 26.4; DB 4; Length 312957;
Best Local Similarity 75.0%; Pred. No. 21;
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DB      129890 GATTGTTTAAACCTTTCAGAGGAGAGAGGTTGCCCTTGATTC 129933

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Search completed: July 13, 2005, 19:44:56
 Job time : 21.2529 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using SW model

Run on: July 13, 2005, 16:24:26 ; Search time 372.764 Seconds
(without alignments)
10269.122 Million cell updates/sec

Title: US-10-804-120-5

Sequence: 1 gtagagtttttcgcgggggtt.....ctatgagcacagtttaca 79

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Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

GenBank:.*
1: gb_ba:.*
2: gb_hcg:.*
3: gb_in:.*
4: gb_om:.*
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6: gb_pat:.*
7: gb_ph:.*
8: gb_pl:.*
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12: gb_sy:.*
13: gb_un:.*
14: gb_vi:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	79	100.0	79	6	AR138936 Sequence
2	79	100.0	79	6	AR544598 Sequence
3	79	100.0	79	6	AX137605 Sequence
4	79	100.0	79	6	AX137726 Sequence
5	79	100.0	79	6	BD006805 L-tycin-P
6	79	100.0	79	6	BD010850 Coryneb
7	77.4	98.0	79	6	AR138935 Sequence
8	77.4	98.0	79	6	AR544597 Sequence
9	77.4	98.0	79	6	AX137604 Sequence
10	77.4	98.0	79	6	AX137725 Sequence
11	77.4	98.0	79	6	BD006804 L-tycin-P
12	77.4	98.0	79	6	BD010849 Coryneb
13	77.4	98.0	1026	6	AX063773 Sequence
14	77.4	98.0	1026	6	AX244061 Sequence
15	77.4	98.0	1341	1	CGDAPAG
16	77.4	98.0	1341	1	CGDAPAG
17	77.4	98.0	1411	6	AR038113 Sequence
18	77.4	98.0	1411	6	AR095435 Sequence
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20	77.4	98.0	1411	6	E14517	E14517 DNA encodin
21	77.4	98.0	1411	6	E16752	E16752 gDNA encodi
22	77.4	98.0	1902	1	CGDAPB	X67737 C.Glutamicu
23	77.4	98.0	3572	1	BLDAPB	221502 B.lactoferm
24	77.4	98.0	337200	1	AP005280	AP005280 Coryneb
25	77.4	98.0	349584	1	EX927153	EX927153 Coryneb
26	77.4	98.0	349980	6	AX127149	AX127149 Sequence
27	77.4	98.0	78.0	80	AR138937	AR138937 Sequence
28	61.6	78.0	80	6	AR544599	AR544599 Sequence
29	61.6	78.0	80	6	AX137606	AX137606 Sequence
30	61.6	78.0	80	6	AX137727	AX137727 Sequence
31	61.6	78.0	80	6	BD006806	BD006806 L-tycin-P
32	61.6	78.0	80	6	BD010851	BD010851 Coryneb
33	48.2	61.0	1333	6	E54479	E54479 Heat-resist
34	48.2	61.0	3063	1	AB083130	AB083130 Coryneb
35	48.2	61.0	303250	1	AP005220	AP005220 Coryneb
36	40	50.6	40	6	AR544607	AR544607 Sequence
37	33.6	42.5	40	6	AR544609	AR544609 Sequence
38	32.6	41.3	39	6	AR544608	AR544608 Sequence
39	30.4	38.5	165921	9	AC009159	AC009159 Homo sapi
40	29.8	37.7	234797	2	AC130921	AC130921 Rattus no
41	29.8	37.7	254796	2	AC097920	AC097920 Rattus no
42	29.6	37.5	213462	10	AC077689	AC077689 Mus Muscu
43	29.6	37.5	219769	10	AC067964	AC067964 Mus Muscu
44	29.4	37.2	148937	2	AC015902	AC015902 Homo sapi
45	29.4	37.2	205000	2	CR533575	CR533575 Danio rer

ALIGNMENTS

RESULT 1	AR138936	Sequence 5 from patent US 6200785.	79 bp	DNA	linear	PAT 16-JUN-2001
LOCUS	AR138936					
DEFINITION	Sequence 5 from patent US 6200785.					
ACCESSION	AR138936					
VERSION	AR138936.1	GI:14481281.				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 79)					
AUTHORS	Kreutzer, C., Hans, S., Rieping, M., Mockel, B., Pfeiffer, W., Eggeling, L., Sahm, H. and Patek, M.					
TITLE	L-lysine-producing corynebacteria and process for the preparation of L-lysine					
JOURNAL	Patent: US 6200785-A 5 13-MAR-2001;					
FEATURES	Location/Qualifiers					
source	1..79					
ORIGIN	/organism="unknown"					
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Gaps	0;			
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DB	1	GTTAGGTTTTTTCGCGGGTTGTTTAA	CCCCCAATGAGGAAAGATGTAACCTTGAACTC	60
QY	61	TATGAGCAGACAGGTTTACA	79	
DB	61	TATGAGCAGACAGGTTTACA	79	
LOCUS	AR544598			
DEFINITION	Sequence 5 from patent US 6746855.			
ACCESSION	AR544598			
VERSION	AR544598.1	GI:53937424		
KEYWORDS				

SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 79)
AUTHORS Kreutzer,C., Hans,S., Rieping,M., Mockel,B., Pfefferle,W., Eggeling,L., Salm,H. and Patek,M.
TITLE L-lysine-producing corynebacteria and process for the preparation of L-lysine
JOURNAL Patent: US 674685-A 5 08-JUN-2004;
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Best Local Similarity 100.0%; Pred. No. 6,4e-17;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTAGGTTTTTGGGGGTTGTTAAACCCCAATGAGGAGATGTTAAGTTGAATC 60
Db 1 GTTAGGTTTTTGGGGGTTGTTAAACCCCAATGAGGAGATGTTAAGTTGAATC 60
QY 61 TATGAGCACAGGTTTAA 79
Db 61 TATGAGCACAGGTTTAA 79

RESULT 3
AX137726 79 bp DNA linear PAT 30-MAY-2001
LOCUS Sequence 5 from Patent EPI067193.
AX137726
VERSION AX137605.1 GI:14273792
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Kreutzer,C., Mockel,B., Pfefferle,W., Eggeling,L., Salm,H. and Patek,M.
TITLE L-lysine producing coryneform bacteria and methods for the production of L-lysine
JOURNAL Patent: EP 1067193-A 5 10-JAN-2001;
FEATURES
source
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/organism="synthetic construct"
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/note="dapA-Promotor von C. glutamicum mit der MC20-Mutation"

ORIGIN
variation
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Query Match 100.0%; Score 79; DB 6; Length 79;
Best Local Similarity 100.0%; Pred. No. 6,4e-17;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GTTAGGTTTTTGGGGGTTGTTAAACCCCAATGAGGAGATGTTAAGTTGAATC 60
QY 61 TATGAGCACAGGTTTAA 79
Db 61 TATGAGCACAGGTTTAA 79

RESULT 4
AX137726 79 bp DNA linear PAT 30-MAY-2001
LOCUS Sequence 5 from Patent EPI067192.
AX137726

VERSION AX137726.1 GI:14273900
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Moedel,B., Pfefferle,W., Kreutzer,C., Hans,S., Rieping,M., Eggeling,L., Salm,H. and Patek,M.
TITLE L-lysine producing coryneform bacteria and methods for the production of L-lysine
JOURNAL Patent: EP 1067192-A 5 10-JAN-2001;
FEATURES
source
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="dapA-Promotor von C. glutamicum mit der MC20-Mutation"

ORIGIN
variation
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Best Local Similarity 100.0%; Pred. No. 6,4e-17;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTAGGTTTTTGGGGGTTGTTAAACCCCAATGAGGAGATGTTAAGTTGAATC 60
Db 1 GTTAGGTTTTTGGGGGTTGTTAAACCCCAATGAGGAGATGTTAAGTTGAATC 60
QY 61 TATGAGCACAGGTTTAA 79
Db 61 TATGAGCACAGGTTTAA 79

RESULT 5
BD006805 79 bp DNA linear PAT 09-JAN-2004
LOCUS L-ricin-productible corynebacteria, replicable DNA among them, process for producing L-ricin, and strains of E. coli and Corynebacterium glutamicum.
BD006805
VERSION BD006805.1 GI:18635176
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 79)
AUTHORS Creutzer,C., Meckel,V., Puffeffare,W., Eggeling,L., Zamu,H. and Patek,M.
TITLE L-ricin-productible corynebacteria, replicable DNA among them, process for producing L-ricin, and strains of E. coli and Corynebacterium glutamicum.
JOURNAL Patent: JP 2001037495-A 4 13-FEB-2001;
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 6.4e-17;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 GTTAGGTTTTTGGCGGGTTGTTAAACCCCAATGAGGAGATGTAACCTTGAATC 60
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QY 61 TATGAGCACAGGTTTAA 79
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DB 61 TATGAGCACAGGTTTAA 79
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RESULT 6
BD010850 79 bp DNA linear PAT 31-JAN-2002
LOCUS
DEFINITION Corynebacterium producing L-ricin and process for producing L-ricin.
ACCESSION BD010850
VERSION BD010850.1 GI:18639223
KEYWORDS JP 2001061485-A/4.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 79)
AUTHORS Meckel,V., Pfefferle,W., Kreuzer,C., Hans,S., Rieping,M., Eggeling,L., Sahm,H. and Patek,M.
Corynebacterium producing L-ricin and process for producing L-ricin
Patent: JP 2001061485-A 4 13-MAR-2001;
DEGUS SA HUELS AG, FORSCHUNGSZENTRUM JUELICH GMBH
COMMENT OS Artificial Sequence
PN JP 2001061485-A/4
PD 13-MAR-2001 JP 2000202551
PR 04-JUL-2000 JP 200202551
PF 07-JUL-1999 DE 19931317.2
PI VETTYNA MECKEL, WALTER PFEFFERLE, CAROLINE CREUZER, STEPHEN HANS, PI MECHTHILD RIEPING, IOTHAAR EGGERING, HERMANN SAHM, PI MIKROSAFUFU PATERKU
PC C12N15/09, C12N1/21, C12P13/08// (C12N15/09, C12R1.15), (C12N1/21, C12R1.15),
PC (C12N1/21, C12R1.19), (C12P13/08, C12R1.15), C12N15/00, (C12N15/00, C12R1.15)
PC CC
FH Key Location/Qualifiers
FT mutation (45).
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source Location/Qualifiers
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/organism="synthetic construct"
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ORIGIN

Query Match 100.0%; Score 79; DB 6; Length 79;
Best Local Similarity 100.0%; Pred. No. 6.4e-17;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTAGGTTTTTGGCGGGTTGTTAAACCCCAATGAGGAGATGTAACCTTGAATC 60
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DB 1 GTTAGGTTTTTGGCGGGTTGTTAAACCCCAATGAGGAGATGTAACCTTGAATC 60
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QY 61 TATGAGCACAGGTTTAA 79
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DB 61 TATGAGCACAGGTTTAA 79
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RESULT 7
AR138935 79 bp DNA linear PAT 16-JUN-2001
LOCUS
DEFINITION Sequence 4 from patent US 6200785.
ACCESSION AR138935
VERSION AR138935.1 GI:14481280

KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 79)
AUTHORS Kreuzer,C., Hans,S., Rieping,M., Meckel,B., Pfefferle,W., Eggeling,L., Sahm,H. and Patek,M.
L-lysine-producing corynebacteria and process for the preparation of L-lysine
Patent: US 6200785-A 4 13-MAR-2001;
JOURNAL Location/Qualifiers
FEATURES
source 1..79
/organism="unknown"
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ORIGIN

Query Match 98.0%; Score 77.4; DB 6; Length 79;
Best Local Similarity 98.7%; Pred. No. 2.4e-16;
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QY 1 GTTAGGTTTTTGGCGGGTTGTTAAACCCCAATGAGGAGATGTAACCTTGAATC 60
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QY 61 TATGAGCACAGGTTTAA 79
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DB 61 TATGAGCACAGGTTTAA 79
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RESULT 8
AR544597 79 bp DNA linear PAT 08-OCT-2004
LOCUS
DEFINITION Sequence 4 from patent US 6746855.
ACCESSION AR544597
VERSION AR544597.1 GI:53937423
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 79)
AUTHORS Kreuzer,C., Hans,S., Rieping,M., Meckel,B., Pfefferle,W., Eggeling,L., Sahm,H. and Patek,M.
L-lysine-producing corynebacteria and process for the preparation of L-lysine
Patent: US 6746855-A 4 08-JUN-2004;
JOURNAL Location/Qualifiers
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ORIGIN

Query Match 98.0%; Score 77.4; DB 6; Length 79;
Best Local Similarity 98.7%; Pred. No. 2.4e-16;
Matches 78; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 61 TATGAGCACAGGTTTAA 79
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DB 61 TATGAGCACAGGTTTAA 79
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RESULT 9
AX137604 79 bp DNA linear PAT 30-MAY-2001
LOCUS
DEFINITION Sequence 4 from patent EP1067193.
ACCESSION AX137604
VERSION AX137604.1 GI:14273791
KEYWORDS Corynebacterium glutamicum
SOURCE Corynebacterium glutamicum

REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source

Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
1
Kreutzer,C., Moeckel,B., Pfeifferle,W., Eggerling,L., Sahm,H. and
Patek,M.
L-lysine producing coryneform bacteria and methods for the
production of L-lysine
Patent: EP 1067193-A 4 10-JAN-2001;
Degussa AG (DE) ; Forschungszentrum Juelich (DE)
Location/Qualifiers
1. .79
/organism="Corynebacterium glutamicum"
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ORIGIN

Query Match 98.0%; Score 77.4; DB 6; Length 79;
Best Local Similarity 98.7%; Pred. No. 2.4e-16;
Matches 78; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTAGGTTTTGGGGGTTTAAACCCCAATGAGGAGAGTGAACCTTGAATC 60
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Db 1 GTTAGGTTTTGGGGGTTTAAACCCCAATGAGGAGAGTGAACCTTGAATC 60
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Qy 61 TATGACACAGGTTTAAACA 79
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Db 61 TATGACACAGGTTTAAACA 79
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RESULT 10
AX137725 79 bp DNA linear PAT 30-MAY-2001
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Sequence 4 from Patent EP1067192.
AX137725
AX137725.1 GI:14273899
Corynebacterium glutamicum
Corynebacterium glutamicum
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
1
Moeckel,B., Pfeifferle,W., Kreutzer,C., Hans,S., Rieping,M.,
Eggerling,L., Sahm,H. and Patek,M.
L-lysine producing coryneform bacteria and methods for the
production of L-lysine
Patent: EP 1067192-A 4 10-JAN-2001;
Degussa AG (DE) ; FORSCHUNGSZENTRUM JUELICH GMBH (DE)
Location/Qualifiers
1. .79
/organism="Corynebacterium glutamicum"
/mol_type="unassigned DNA"
/db_xref="taxon:1718"
/note="dapa Wildtyp-Promotor"

ORIGIN

Query Match 98.0%; Score 77.4; DB 6; Length 79;
Best Local Similarity 98.7%; Pred. No. 2.4e-16;
Matches 78; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTAGGTTTTGGGGGTTTAAACCCCAATGAGGAGAGTGAACCTTGAATC 60
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Db 1 GTTAGGTTTTGGGGGTTTAAACCCCAATGAGGAGAGTGAACCTTGAATC 60
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Qy 61 TATGACACAGGTTTAAACA 79
|||||
Db 61 TATGACACAGGTTTAAACA 79
|||||

RESULT 11
BD006804 79 bp DNA linear PAT 31-JAN-2002
LOCUS
DEFINITION

BD006804 79 bp DNA linear PAT 31-JAN-2002
L-ricin-productible corynebacteria, replicable DNA among them,

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Process for producing L-ricin, and strains of E. coli and
Corynebacterium glutamicum.
BD006804
BD006804.1 GI:18635175
JP 2001037495-A/3.
Corynebacterium glutamicum
Corynebacterium glutamicum
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
1 (bases 1 to 79)
Kreutzer,C., Meckel,V., Pfeifferle,W., Eggerling,L., Zamu,H. and
Pateku,M.
L-ricin-productible corynebacteria, replicable DNA among them,
process for producing L-ricin, and strains of E. coli and
Patent: JP 2001037495-A 3 13-FEB-2001;
DEGUSHA HUELS AG,FORSCHUNGSZENTRUM JUELICH GMBH
OS Corynebacterium glutamicum
PN JP 2001037495-A/3
PD 13-FEB-2001
PF 04-JUL-2000 JP 2000202550
PR 07-JUL-1999 DE 19931314.8
PI CAROLINE CREUZER, VETTVANA MECKEL, WALTHER PUEFFARE, PI LOTMAR
EGGERLING,
PI HERMANN ZAMU MIROSUJAFU PATEKU
PC C12N15/09,C12N1/21,C12P13/08//C12N1/21,C12R1:15), (C12N1/21,
PC C12R1:19),
PC (C12P13/08,C12R1:15), C12N15/00
CC
FH Key Location/Qualifiers
FT source 1. .79
/organism="Corynebacterium glutamicum".
Location/Qualifiers
1. .79
/organism="Corynebacterium glutamicum"
/mol_type="genomic DNA"
/db_xref="taxon:1718"

ORIGIN

Query Match 98.0%; Score 77.4; DB 6; Length 79;
Best Local Similarity 98.7%; Pred. No. 2.4e-16;
Matches 78; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTAGGTTTTGGGGGTTTAAACCCCAATGAGGAGAGTGAACCTTGAATC 60
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Db 1 GTTAGGTTTTGGGGGTTTAAACCCCAATGAGGAGAGTGAACCTTGAATC 60
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Qy 61 TATGACACAGGTTTAAACA 79
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Db 61 TATGACACAGGTTTAAACA 79
|||||

RESULT 12
BD010849 79 bp DNA linear PAT 31-JAN-2002
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BD010849 79 bp DNA linear PAT 31-JAN-2002
Corynebacterium producing L-ricin and process for producing
L-ricin.
BD010849
BD010849.1 GI:18639222
JP 2001061485-A/3.
Corynebacterium glutamicum
Corynebacterium glutamicum
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
1 (bases 1 to 79)
Meckel,V., Pfeifferle,W., Creuzer,C., Hans,S., Rieping,M.,
Eggerling,L., Sahm,H. and Pateku,M.
Corynebacterium producing L-ricin and process for producing L-ricin
Patent: JP 2001061485-A 3 13-MAR-2001;
DEGUSHA HUELS AG,FORSCHUNGSZENTRUM JUELICH GMBH
OS Corynebacterium glutamicum
PN JP 2001061485-A/3
PD 13-MAR-2001
PF 04-JUL-2000 JP 2000202551

```

PR 07-JUL-1999 DE 19931317.2
PI VERTYVA MECKEL, WALTER PEEFERLE, CAROLINE CREUZER, STEPHEN HANS,
PI MECHTILD RIEPING, IOTHA RIEGERING, HERMANN SAHM, PI
MIROSRAPU PATEKU
PC C12N15/09, C12N1/21, C12P13/08 // (C12N15/09, C12R1:15), (C12N1/21,
PC C12R1:15),
PC (C12N1/21, C12R1:19), (C12P13/08, C12R1:15), C12N15/00, (C12N15/00,
PC C12R1:15)
CC
CC
FH Key Location/Qualifiers
FT Source 1..79
FT /organism='Corynebacterium glutamicum'.
FT Location/Qualifiers
1..79
/organism='Corynebacterium glutamicum'
/mol_type='genomic DNA'
/db_xref='taxon:1718'

ORIGIN
Query Match 98.0%; Score 77.4; DB 6; Length 79;
Best Local Similarity 98.7%; Pred. No. 2.4e-16;
Matches 78; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTAGGTTTTTCGGGGTGTGTTAAACCCCAATGAGGAGATGTAACCTTGAATC 60
DB 1 GTTAGGTTTTTCGGGGTGTGTTAAACCCCAATGAGGAGATGTAACCTTGAATC 60

QY 61 TATGACACAGGTTTAA 79
DB 61 TATGACACAGGTTTAA 79

RESULT 13
LOCUS AX063773 1026 bp DNA linear PAT 24-JAN-2001
DEFINITION Sequence 55 from Patent WO0100843.
ACCESSION AX063773
VERSION AX063773.1 GI:12541485
KEYWORDS
SOURCE Corynebacterium glutamicum
ORGANISM Corynebacterium glutamicum
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.

REFERENCE
1 Pompejus, M., Kroege, B., Schroeder, H., Zelder, O. and Haberer, G.
corynebacterium glutamicum genes encoding metabolic pathway
proteins
Patent: WO 0100843-A 55 04-JAN-2001;
BASF AKTIENGESSELLSCHAFT (DE)
Location/Qualifiers
1..1026
/organism='Corynebacterium glutamicum'
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/db_xref='taxon:1718'
101..1006
/note='unnamed protein product; RXA00865'
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/protein_id='CAC25128.1'
/db_xref='GI:12541486'
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RRLSELPTLIVAKDKDLVAATSLIKETGLAAYSGDDPLNVLWALGSGGTSVIGH
AAPTLRELVTSEEGDLVRAEINAKSLPLVAAGRLGVSIAKALRLQGINVGD
RPIMAPNEOELEALREDMKAGVL'

ORIGIN
Query Match 98.0%; Score 77.4; DB 6; Length 1026;
Best Local Similarity 98.7%; Pred. No. 1.9e-16;
Matches 78; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTAGGTTTTTCGGGGTGTGTTAAACCCCAATGAGGAGATGTAACCTTGAATC 60
DB 40 GTTAGGTTTTTCGGGGTGTGTTAAACCCCAATGAGGAGATGTAACCTTGAATC 99

QY 61 TATGACACAGGTTTAA 79
DB 61 TATGACACAGGTTTAA 79

QY 100 TATGACACAGGTTTAA 118
DB 100 TATGACACAGGTTTAA 118

RESULT 14
LOCUS AX244061 1026 bp DNA linear PAT 28-SEP-2001
DEFINITION Sequence 53 from Patent WO0166573.
ACCESSION AX244061
VERSION AX244061.1 GI:15859125
KEYWORDS
SOURCE Corynebacterium glutamicum
ORGANISM Corynebacterium glutamicum
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.

REFERENCE
1 Pompejus, M., Kroege, B., Schroeder, H., Zelder, O., Haberer, G.,
Kim, J.W., Lee, H.S. and Hwang, B.J.
Corynebacterium glutamicum genes encoding metabolic pathway
proteins
Patent: WO 0166573-A 53 13-SEP-2001;
BASF AKTIENGESSELLSCHAFT (DE)
Location/Qualifiers
1..1026
/organism='Corynebacterium glutamicum'
/mol_type='unassigned DNA'
/db_xref='taxon:1718'
101..1006
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/codon_start=1
/transl_table=11
/protein_id='CAC88509.1'
/db_xref='GI:15859126'
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AASAGADGLIVTPYKRSQGLAHRAITAEVPCIDYIGRSGIPESDTM
RRLSELPTLIVAKDKDLVAATSLIKETGLAAYSGDDPLNVLWALGSGGTSVIGH
AAPTLRELVTSEEGDLVRAEINAKSLPLVAAGRLGVSIAKALRLQGINVGD
RPIMAPNEOELEALREDMKAGVL'

ORIGIN
Query Match 98.0%; Score 77.4; DB 6; Length 1026;
Best Local Similarity 98.7%; Pred. No. 1.9e-16;
Matches 78; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTAGGTTTTTCGGGGTGTGTTAAACCCCAATGAGGAGATGTAACCTTGAATC 60
DB 40 GTTAGGTTTTTCGGGGTGTGTTAAACCCCAATGAGGAGATGTAACCTTGAATC 99

QY 61 TATGACACAGGTTTAA 79
DB 61 TATGACACAGGTTTAA 79

QY 100 TATGACACAGGTTTAA 118
DB 100 TATGACACAGGTTTAA 118

RESULT 15
LOCUS AJ584662 1341 bp DNA linear BCT 04-OCT-2003
DEFINITION Corynebacterium glutamicum dapA gene for dihydrodipicolinate
synthetase.
ACCESSION AJ584662
VERSION AJ584662.1 GI:37515386
KEYWORDS
SOURCE Corynebacterium glutamicum
ORGANISM Corynebacterium glutamicum
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.

REFERENCE
1 Vu Kim, T., Le Ian, H., Duong Hong, Q., Nguyen Thuy, C. and Dinh Duy, K.
Cloning of the gene coding for dihydrodipicolinate synthetase from

```

JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

Corynebacterium glutamicum HN30 isolate
Unpublished
2 (bases 1 to 1341)
Dinh Duy, K.
Direct Submission
Submitted (01-OCT-2003) Dinh Duy K., Molecular Microbiology Lab,
Institute of Biotechnology, NCST, 18, Hoang Quoc Viet, Cau Giay,
Hanoi, 10000, VIET NAM

FEATURES
SOURCE

Location/Qualifiers
1..1341
/organism="Corynebacterium glutamicum"
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/isolate="HN30"
/db_xref="taxon:1718"
249..1154
/gene="dapa"
249..1154
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/codon_start=1
/transl_table=1
/product="dihydrodipicolinate synthetase"
/protein_id="CAE48279.1"
/db_xref="GI:37515387"
/translation="MSTGLTAKGVHEHGVAVMTPTESGDIDIAGREVAAYLV
DKGIDSLVLAGTGESPTTAARELLKAVREVGDRKLIAGVGTNNRTSVELAE
AASAGADGLIVTPYYSKPSQBSGLAHFGAIAAATEVPICVDIPRSGIPESDTM
RRSELPTIIAVDKAGDLVAATSLIKETGLAMVSGDDPLNLVWLALGSSGFISVIGH
AAPTAARELYTSFEESDLYRAREINAKLSPLVAAQRLGGVSLAKAASRLQGINVQDP
RLPTMAENEQLEALREDMKKAGVL"

ORIGIN

Query Match 98.0%; Score 77.4; DB 1; Length 1341;
Best Local Similarity 98.7%; Pred. No. 1.9e-16;
Matches 78; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GTTAGTTTTTGGGGGTTTAACCCCAATGAGGAGATGTTAACTTGAAGTC 60
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Db 188 GTTAGTTTTTGGGGGTTTAACCCCAATGAGGAGATGTTAACTTGAAGTC 247
|||
QY 61 TATGACACAGTTTAAACA 79
|||
Db 248 TATGACACAGTTTAAACA 266
|||

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Job time : 376.764 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 13, 2005, 15:18:23 ; Search time 62.0069 Seconds
(without alignments)
7542.061 Million cell updates/sec

Title: US-10-804-120-5

Perfect score: 79

Sequence: 1 gttaggcttttcgcgggggtt.....ctatgagcacaggtttaca 79

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
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11: geneseqn2003ds:*
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13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	79	100.0	79	AAf26007	Aaf26007 C. glutam
2	79	100.0	79	AAf26024	Aaf26024 C. glutam
3	77.4	98.0	79	AAf26006	Aaf26006 C. glutam
4	77.4	98.0	79	AAf26023	Aaf26023 C. glutam
5	77.4	98.0	1026	AAf71780	Aaf71780 Coryneb
6	77.4	98.0	1026	AAf26009	Aaf26009 C. glutam
7	77.4	98.0	1411	AAf84782	Aaf84782 Brevibact
8	77.4	98.0	1411	AAf49281	Aaf49281 DNA encod
9	77.4	98.0	1411	AAf40256	Aaf40256 Brevibact
10	77.4	98.0	1411	AAfV5785	AafV5785 B. lactof
11	77.4	98.0	349980	AAf68530	Aaf68530 C. glutam
12	77.4	98.0	80	AAf26008	Aaf26008 C. glutam
13	77.4	98.0	80	AAf26025	Aaf26025 C. glutam
14	48.2	61.0	1333	AAf45371	Aaf45371 C. thermo
15	40	50.6	40	AAf26001	Aaf26001 C. glutam
16	40	50.6	40	AAf26018	Aaf26018 C. glutam
17	33.6	42.5	40	AAf26003	Aaf26003 C. glutam
18	33.6	42.5	40	AAf26020	Aaf26020 C. glutam
19	32.6	41.3	39	AAf26002	Aaf26002 C. glutam
20	32.6	41.3	39	AAf26019	Aaf26019 C. glutam

C	21	28.4	35.9	30	6	AB079593	Abg79593 Dihydrodi
	22	28.2	35.7	47115	9	AD02627	Ad02627 Mouse Flt
	23	28.2	35.7	47115	10	ADB72365	ADB72365 Mouse Flt
	24	28.2	35.7	47115	10	ADB95875	ADB95875 Mouse Flt
C	25	27.4	34.7	320	5	ABV61096	ABv61096 Human pro
	26	27.2	34.4	36	4	AAf26000	Aaf26000 C. glutam
	27	27.2	34.4	36	4	AAf26017	Aaf26017 C. glutam
	28	26.6	33.7	2193	13	AD545856	Ad545856 Bacterial
	29	26.6	33.7	29220	4	AAf27653	Aaf27653 DNA encod
C	30	26.6	33.7	29220	4	AAf27652	Aaf27652 DNA encod
	31	26.6	33.7	29220	10	ADB94455	ADB94455 Novel hum
	32	26.6	33.7	29220	10	ADB94456	ADB94456 Novel hum
	33	26.6	33.4	321019	13	AD536450	Ad536450 Human aut
	34	26.4	33.4	329019	13	ABD32707	ABd32707 Human can
	35	26.2	33.2	609	13	ADO52661	AdO52661 Novel can
	36	26	32.9	618	8	ACA00742	AcA00742 C. glutam
	37	26	32.9	1102	13	AD517012	Ad517012 B. lichen
	38	26	32.9	1102	13	AD517014	Ad517014 B. lichen
C	39	26	32.9	349980	5	AAf68531	Aaf68531 C. glutam
C	40	25.6	32.4	545	6	ABf67098	Abf67098 Thyroid c
C	41	25.6	32.4	545	6	ABf68951	Abf68951 Kidney ca
	42	25.4	32.2	1071	4	ABA88963	AbA88963 Escherich
	43	25.4	32.2	13714	6	ABf79040	Abf79040 E. coli C
	44	25.4	32.2	13714	10	ADH80607	AdH80607 Escherich
	45	25.4	32.2	13757	4	ABA88957	AbA88957 Escherich

ALIGNMENTS

RESULT 1	AAf26007	AAf26007 standard; DNA; 79 BP.
ID	AAf26007	
XX	AAf26007;	
AC	AAf26007;	
XX		
DT	20-APR-2001 (first entry)	
XX		
DE	C. glutamicum dapA mutant MC20 promoter DNA fragment SEQ ID 5.	
XX		
KM	lysE, L-lysine, lysine exporter-carrier; dapA; aspartate kinase; lysC;	
KW	dihydropicolinate synthase; pyc; pyruvate carboxylase; dapB; promoter;	
KM	dihydropicolinate reductase; fdder additive; ss.	
XX		
OS	Corynebacterium glutamicum.	
XX		
PN	.EP1067192-A1.	
XX		
PD	10-JAN-2001.	
XX		
PF	06-JUL-2000; 2000EP-00114501.	
XX		
PR	07-JUL-1999; 99DE-01031317.	
XX		
PA	(DEGS) DEGUSSA-HUELS AG.	
XX	(KERJ) FORSCHUNGSZENTRUM JUELICH GMBH.	
PI	Moekkel B, Pfeifferle W, Kreutzer C, Hans S, Rieping M;	
XX	Begging L, Sahn H, Patek M;	
DR	WPI; 2001-125731/14.	
XX		
PT	Coryneform bacteria for high level production of lysine, useful as feed	
PT	additive, overexpresses the lysE and at least one other gene,	
XX	particularly dapA.	
PS	Claim 4; Page 17; 25pp; German.	
XX		
CC	This invention describes a novel L-lysine producing coryneform bacterium	
CC	(A) with an amplified lysE (lysine exporter-carrier) gene in which at	
CC	least one of the additional genes dapA (dihydropicolinate synthase), lysC	
CC	(aspartate kinase), pyc (pyruvate carboxylase) and/or dapB	
CC	(dihydropicolinate reductase) is amplified and preferably overexpressed.	

CC L-lysine is used as a fodder additive for animals. Overexpression of the
 CC additional genes improves lysine production compared with amplification
 CC of lysE only. Corynebacterium glutamicum DSM 5715 transformed with
 CC vectors that overexpress (i) dapA and (ii) both lysE and dapB produced
 CC lysine hydrochloride at 15.4 g/l after 48 hr culture at 33plusoc. The
 CC same strain that overexpressed lysE only produced 11.1 g/l
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 SQ Sequence 79 BP, 21 A; 13 C; 21 G; 24 T; 0 U; 0 Other;
 Query Match 100.0%; Score 79; DB 4; Length 79;
 Best Local Similarity 100.0%; Pred. No. 1.1e-19;
 Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GTTAGGTTTTTGGGGGTTTAAACCCCAATGAGGAGATGTGAACCTTGAATC 60
 DB 1 GTTAGGTTTTTGGGGGTTTAAACCCCAATGAGGAGATGTGAACCTTGAATC 60
 QY 61 TATGACACAGGTTTAAACA 79
 DB 61 TATGACACAGGTTTAAACA 79
 RESULT 2
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 ID AAF26024 standard; DNA; 79 BP.
 XX
 AC AAF26024;
 XX
 DT 20-APR-2001 (first entry)
 XX
 DE C. glutamicum dapA MC20 mutant promoter fragment SEQ ID 5.
 XX
 KW lysE; L-lysine; pyc; pyruvate carboxylase; dapA; lysine exporter-carrier;
 KW dihydrodipicolinate synthase; lysC; aspartate kinase; lysB; dapB;
 KW dihydrodipicolinate reductase; fodder additive; ss.
 XX
 OS Corynebacterium glutamicum.
 XX
 PN EP1067193-A1.
 XX
 PD 10-JAN-2001.
 XX
 PF 06-JUL-2000; 2000EP-00114502.
 XX
 PR 07-JUL-1999; 99DE-01031314.
 XX
 PA (DEGS) DEGUSA-HUELS AG.
 PA (KERJ) FORSCHUNGSZENTRUM JUELICH.
 XX
 PI Kreutzner C, Moessel B, Pfeifferle W, Eggeling L, Sahn H, Patek M;
 XX
 DR WPI; 2001-140055/15.
 XX
 PT Coryneform bacteria for high level production of lysine, useful as feed
 PT additive, overexpresses the pyc and at least one other gene, e.g. dapA,
 PT dapB or lysE.
 XX
 PS Claim 4; Page 20; 28pp; German.
 XX
 CC This invention describes a novel L-lysine producing coryneform bacterium
 CC (A) with an amplified pyc (pyruvate carboxylase) gene in which at least
 CC one of the additional genes dapA (dihydrodipicolinate synthase), lysC
 CC (aspartate kinase), lysB (lysine exporter-carrier) and/or dapB
 CC (dihydrodipicolinate reductase) is amplified and preferably overexpressed.
 CC L-lysine is used as a fodder additive for animals. Overexpression of the
 CC additional genes improves lysine production compared with amplification
 CC of pyc only. Corynebacterium glutamicum DSM 5715 transformed with vectors
 CC that overexpress dapA and all of pyc, lysE and dapB produced lysine
 CC hydrochloride at 17.6 g/l after 72 hr culture at 33plusoc. The same
 CC strain that overexpressed pyc only produced 11.3 g/l
 XX
 SQ Sequence 79 BP, 21 A; 13 C; 21 G; 24 T; 0 U; 0 Other;

Query Match 100.0%; Score 79; DB 4; Length 79;
 Best Local Similarity 100.0%; Pred. No. 1.1e-19;
 Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GTTAGGTTTTTGGGGGTTTAAACCCCAATGAGGAGATGTGAACCTTGAATC 60
 DB 1 GTTAGGTTTTTGGGGGTTTAAACCCCAATGAGGAGATGTGAACCTTGAATC 60
 QY 61 TATGACACAGGTTTAAACA 79
 DB 61 TATGACACAGGTTTAAACA 79
 RESULT 3
 AAF26006
 ID AAF26006 standard; DNA; 79 BP.
 XX
 AC AAF26006;
 XX
 DT 20-APR-2001 (first entry)
 XX
 DE C. glutamicum dapA wild-type promoter DNA fragment SEQ ID 4.
 XX
 KW lysE; L-lysine; lysine exporter-carrier; dapA; aspartate kinase; lysC;
 KW dihydrodipicolinate synthase; pyc; pyruvate carboxylase; dapB; promoter;
 KW dihydrodipicolinate reductase; fodder additive; ss.
 XX
 OS Corynebacterium glutamicum.
 XX
 PN EP1067192-A1.
 XX
 PD 10-JAN-2001.
 XX
 PF 06-JUL-2000; 2000EP-00114501.
 XX
 PR 07-JUL-1999; 99DE-01031317.
 XX
 PA (DEGS) DEGUSA-HUELS AG.
 PA (KERJ) FORSCHUNGSZENTRUM JUELICH GMBH.
 XX
 PI Moessel B, Pfeifferle W, Kreutzner C, Hans S, Rieping M;
 XX
 DR WPI; 2001-125731/14.
 XX
 PT Coryneform bacteria for high level production of lysine, useful as feed
 PT additive, overexpresses the lysE and at least one other gene,
 PT particularly dapA.
 XX
 PS Disclosure; Page 17; 25pp; German.
 XX
 CC This invention describes a novel L-lysine producing coryneform bacterium
 CC (A) with an amplified lysE (lysine exporter-carrier) gene in which at
 CC least one of the additional genes dapA (dihydrodipicolinate synthase), lysC
 CC (aspartate kinase), pyc (pyruvate carboxylase) and/or dapB
 CC (dihydrodipicolinate reductase) is amplified and preferably overexpressed.
 CC L-lysine is used as a fodder additive for animals. Overexpression of the
 CC additional genes improves lysine production compared with amplification
 CC of lysE only. Corynebacterium glutamicum DSM 5715 transformed with
 CC vectors that overexpress (i) dapA and (ii) both lysE and dapB produced
 CC lysine hydrochloride at 15.4 g/l after 48 hr culture at 33plusoc. The
 CC same strain that overexpressed lysE only produced 11.1 g/l
 XX
 SQ Sequence 79 BP, 22 A; 13 C; 21 G; 23 T; 0 U; 0 Other;
 Query Match 98.0%; Score 77.4; DB 4; Length 79;
 Best Local Similarity 98.7%; Pred. No. 4.2e-19;
 Matches 78; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GTTAGGTTTTTGGGGGTTTAAACCCCAATGAGGAGATGTGAACCTTGAATC 60
 DB 1 GTTAGGTTTTTGGGGGTTTAAACCCCAATGAGGAGATGTGAACCTTGAATC 60

OY 61 TATGACACAGGTTTAAACA 79
 DB 61 TATGACACAGGTTTAAACA 79

RESULT 4
 AAF26023
 ID AAF26023 standard; DNA; 79 BP.

AA26023;

20-APR-2001 (first entry)

C. glutamicum dapa wild type promoter fragment SEQ ID 4.

lysB; L-lysine; pyc; pyruvate carboxylase; dapa; lysine exporter-carrier;
 dihydrodipicolinate synthase; lysC; aspartate kinase; lysB; dapa;
 dihydrodipicolinate reductase; fadder additive; ss.

Corynebacterium glutamicum.

EP1067193-A1.

10-JAN-2001.

06-JUL-2000; 2000EP-00114502.

07-JUL-1999; 99DE-01031314.

(DEGS) DEGUSSA-HUELS AG.
 (KERJ) FORSCHUNGSZENTRUM JUELICH.

Kreuzer C, Moeckel B, Pfefferle W, Eggeling L, Sahn H, Patek M;

WPI; 2001-140055/15.

Coryneform bacteria for high level production of lysine, useful as feed
 additive, overexpresses the pyc and at least one other gene, e.g. dapa,
 dapa or lysB.

disclosure; Page 20; 28pp; German.

This invention describes a novel L-lysine producing coryneform bacterium
 (A) with an amplified pyc (pyruvate carboxylase) gene in which at least
 one of the additional genes dapa (dihydrodipicolinate synthase) lysC
 (aspartate kinase), lysB (lysine exporter-carrier) and/or dapa
 (dihydrodipicolinate reductase) is amplified and preferably overexpressed.
 L-lysine is used as a fodder additive for animals. Overexpression of the
 additional genes improves lysine production compared with amplification
 of pyc only. Corynebacterium glutamicum DSM 5715 transformed with vectors
 that overexpress dapa and all of pyc, lysB and dapa produced lysine
 hydrochloride at 17.6 g/l after 72 hr culture at 35pluoc. The same
 strain that overexpressed pyc only produced 11.3 g/l

Sequence 79 BP; 22 A; 13 C; 21 G; 23 T; 0 U; 0 Other;

Query Match 98.0%; Score 77.4; DB 4; Length 79;
 Best Local Similarity 98.7%; Pred. No. 4.2e-19;
 Matches 78; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GTTAGGTTTTCGCGGTTTAAACCCCAATGAGGAGAGATGTAACCTTGAATC 60
 DB 1 GTTAGGTTTTCGCGGTTTAAACCCCAATGAGGAGAGATGTAACCTTGAATC 60

OY 61 TATGACACAGGTTTAAACA 79
 DB 61 TATGACACAGGTTTAAACA 79

RESULT 5
 AAF71780
 ID AAF71780 standard; DNA; 1026 BP.
 XX

AC AAF71780;

30-APR-2001 (first entry)

Corynebacterium glutamicum MP protein nucleotide sequence SEQ ID NO:55.

Corynebacterium glutamicum; metabolic pathway protein; MP protein;
 fine chemical production; microorganism; organic acid; nucleoside;
 nonproteinogenic amino acid; purine base; pyrimidine base; nucleotide;
 lipid; saturated fatty acid; unsaturated fatty acid; diol; vitamin;
 carbohydrate; aromatic compound; cofactor; polypeptide; enzyme; ds.

Corynebacterium glutamicum.

WO200100843-A2.

04-JAN-2001.

23-JUN-2000; 2000WO-IB000923.

25-JUN-1999; 99US-0141031P.

01-JUL-1999; 99DE-01030476.

02-JUL-1999; 99US-0142101P.

08-JUL-1999; 99DE-01031415.

08-JUL-1999; 99DE-01031418.

08-JUL-1999; 99DE-01031419.

08-JUL-1999; 99DE-01031420.

08-JUL-1999; 99DE-01031424.

08-JUL-1999; 99DE-01031428.

08-JUL-1999; 99DE-01031433.

08-JUL-1999; 99DE-01031443.

08-JUL-1999; 99DE-01031453.

08-JUL-1999; 99DE-01031457.

08-JUL-1999; 99DE-01031465.

08-JUL-1999; 99DE-01031478.

08-JUL-1999; 99DE-01031510.

08-JUL-1999; 99DE-01031541.

08-JUL-1999; 99DE-01031573.

08-JUL-1999; 99DE-01031592.

08-JUL-1999; 99DE-01031632.

08-JUL-1999; 99DE-01031634.

08-JUL-1999; 99DE-01031636.

08-JUL-1999; 99DE-01032125.

08-JUL-1999; 99DE-01032126.

08-JUL-1999; 99DE-01032130.

08-JUL-1999; 99DE-01032186.

08-JUL-1999; 99DE-01032206.

08-JUL-1999; 99DE-01032227.

08-JUL-1999; 99DE-01032228.

08-JUL-1999; 99DE-01032229.

08-JUL-1999; 99DE-01032230.

08-JUL-1999; 99DE-01032922.

08-JUL-1999; 99DE-01032926.

08-JUL-1999; 99DE-01032928.

08-JUL-1999; 99DE-01033004.

08-JUL-1999; 99DE-01033005.

08-JUL-1999; 99DE-01033006.

08-JUL-1999; 99US-0148613P.

08-JUL-1999; 99DE-01040764.

08-JUL-1999; 99DE-01040765.

08-JUL-1999; 99DE-01040766.

08-JUL-1999; 99DE-01040832.

08-JUL-1999; 99DE-01041378.

08-JUL-1999; 99DE-01041379.

08-JUL-1999; 99DE-01041380.

08-JUL-1999; 99DE-01041394.

08-JUL-1999; 99DE-01041396.

08-JUL-1999; 99DE-01042076.

08-JUL-1999; 99DE-01042077.

08-JUL-1999; 99DE-01042079.

08-JUL-1999; 99DE-01042086.

08-JUL-1999; 99DE-01042087.

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PR 03-SEP-1999; 99DE-01042088.
PR 03-SEP-1999; 99DE-01042085.
PR 03-SEP-1999; 99DE-01042124.
PR 03-SEP-1999; 99DE-01042129.
PR 09-MAR-2000; 2000US-0187970P.
XX
PA (BAD1 ) BASF AG.
XX
PI Pompejus M, Kroegeer B, Schroeder H, Zelder O, Haberhauer G;
XX
DR WPI; 2001-137957/14.
DR P-PSDB; AAB79661.
XX
XX Nucleic acids from Corynebacterium glutamicum encoding metabolic pathway
PT proteins, useful for producing fine chemicals in microorganisms,
PT including organic acids, nonproteinogenic amino acids, and purine and
PT pyrimidine bases.
XX
XX Claim 3; Page 235-237; 1737pp; English.
XX
CC AAF71753 to AAF72330 encode the Corynebacterium glutamicum metabolic
CC pathway (MP) proteins given in AAB79634 to AAB80211. The C. glutamicum MP
CC nucleic acids are useful for the production of fine chemicals in
CC microorganisms, including organic acids, nonproteinogenic amino acids,
CC purine and pyrimidine bases, nucleosides, nucleotides, lipids, saturated
CC and unsaturated fatty acids, diols, carbohydrates, aromatic compounds,
CC vitamins, cofactors, polyketides and enzymes
CC
XX Sequence 1026 BP; 249 A; 243 C; 283 G; 251 T; 0 U; 0 Other;
SQ
Query Match 98.0%; Score 77.4; DB 4; Length 1026;
Best Local Similarity 98.7%; Pred. No. 9.2e-19;
Matches 78; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GTTAGGTTTTTGGGGGTTTAAACCCCAATGAGGAGAGTGAACCTTGAATC 60
Db 40 GTTAGGTTTTTGGGGGTTTAAACCCCAATGAGGAGAGTGAACCTTGAATC 99
Qy 61 TATGAGCAGCGTTTAA 79
Db 100 TATGAGCAGCGTTTAA 118
XX
RESULT 6
AAS96099 standard; DNA; 1026 BP.
XX
AC AAS96099;
XX
DT 26-FEB-2002 (first entry)
XX
DE C. glutamicum gene #24 encoding metabolic pathway protein.
XX
KM Metabolic pathway protein; MP; lysine biosynthesis pathway;
KM methionine biosynthesis pathway; large-scale production of fine chemical;
KM Corynebacterium diptheriae; diptheria; ds.
XX
OS Corynebacterium glutamicum.
XX
PN WO200166573-A2.
XX
PD 13-SEP-2001.
XX
PF 22-DEC-2000; 2000WO-IB002035.
XX
PR 09-MAR-2000; 2000US-0187970P.
PR 23-JUN-2000; 2000US-00606740.
XX
PA (BAD1 ) BASF AG.
XX
PI Pompejus M, Kroegeer B, Schroeder H, Zelder O, Haberhauer G;
PI Kim J, Lee H, Hwang B;
XX

```

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DR WPI; 2001-582269/65.
DR P-PSDB; AAU71889.
XX
XX Nucleic acids encoding metabolic pathway proteins from Corynebacterium
PT glutamicum, useful for producing methionine and lysine in Corynebacterium
PT and Brevibacterium.
XX
XX Disclosure; Page 216-217; 316pp; English.
XX
PS The present invention relates to the isolation of novel Corynebacterium
XX glutamicum genes encoding metabolic pathway (MP) proteins (AAU71863-
CC AAU71922). The metabolic pathway proteins of the invention include
CC enzymes involved in the lysine and methionine biosynthetic pathways. The
CC polynucleotide sequences of the invention can be used for the large-scale
CC production and/or modulation of expression of fine chemicals such as
CC lysine and methionine. The sequences of the invention may be used to
CC identify C. glutamicum and related organisms e.g. C. diptheriae in a
CC subject to detect diptheria. AAS96073-AAS96132 represent C. glutamicum
CC genes encoding the novel metabolic pathway proteins of the invention
XX
XX Sequence 1026 BP; 249 A; 243 C; 283 G; 251 T; 0 U; 0 Other;
SQ
Query Match 98.0%; Score 77.4; DB 4; Length 1026;
Best Local Similarity 98.7%; Pred. No. 9.2e-19;
Matches 78; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GTTAGGTTTTTGGGGGTTTAAACCCCAATGAGGAGAGTGAACCTTGAATC 60
Db 40 GTTAGGTTTTTGGGGGTTTAAACCCCAATGAGGAGAGTGAACCTTGAATC 99
Qy 61 TATGAGCAGCGTTTAA 79
Db 100 TATGAGCAGCGTTTAA 118
XX
RESULT 7
AAT84782 standard; DNA; 1411 BP.
XX
AC AAT84782;
XX
DT 17-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 10-NOV-1997 (first entry)
XX
DE Brevibacterium lactofermentum dihydrodipicolinate synthase gene.
XX
KM Insertion sequence; transposable element; Coryneform; bacterium;
KM bacteria; amplification; artificial transposon; inverted repeat;
KM amino acid; biosynthesis; aspartokinase; dihydrodipicolinic acid;
KM synthetase; synthase; dihydrodipicolinate; ds.
XX
OS Corynebacterium glutamicum.
XX
PN EP756007-A2.
XX
PD 29-JAN-1997.
XX
PF 28-JUN-1996; 96EP-00110491.
XX
PR 30-JUN-1995; 95JP-00166541.
XX
PA (AJIN ) AJINOMOTO KK.
XX
PI Moriya M, Matsui H, Yokozeki K, Hirano S, Hayakawa A, Izui M;
PI Sugimoto M;
XX
DR WPI; 1997-101858/10.

```


DR P-PSDB; AAW23283.
 XX Amplifying gene, esp. aspartokinase, in Coryneform chromosome using
 PT artificial transposon - useful for amino acid synthesis, esp. lysine.
 XX
 PS Example 5; Page 74-78; 122pp; English.
 XX
 CC The present sequence is a 1.5 kb chromosomal DNA region encoding the
 CC Brevibacterium lactofermentum dihydrodipicolinate synthase. The fragment
 CC can be used in a novel method for the amplification of a desired gene,
 CC comprising the formation of an artificial transposon having a structure
 CC such that a drug resistance gene and the desired gene are held between
 CC inverted repeats. The artificial transposon, which is transposable in a
 CC Coryneform bacterium, is transduced into a Coryneform bacterium,
 CC transposed into its chromosome and the desired gene transduced and
 CC amplified in the chromosome. A transposase gene is preferably held
 CC between the inverted repeats, which are derived from an insertion
 CC sequence of a Coryneform bacterium. The drug resistance gene is the
 CC chloramphenicol or tetracycline resistance gene, and the desired gene is
 CC one that participates in amino acid biosynthesis, especially an
 CC aspartokinase and/or dihydrodipicolinate synthase gene. (Updated on
 CC 25-MAR-2003 to correct PA field.) (Updated on 17-OCT-2003 to standardise
 CC OS field)
 CC
 SQ Sequence 1411 BP; 360 A; 343 C; 374 G; 334 T; 0 U; 0 Other;
 XX
 Query Match 98.0%; Score 77.4; DB 2; Length 1411;
 Best Local Similarity 98.7%; Pred. No. 1e-18; 1; Indels 0; Gaps 0;
 Matches 78; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GTTAGGTTTTTTCGGGGGTTGTTTAAACCCCAATGAGGAGAGTGAACCTTGAATC 60
 DB 250 GTTAGGTTTTTTCGGGGGTTGTTTAAACCCCAATGAGGAGAGTGAACCTTGAATC 309
 QY 61 TATGACACAGGTTTAAACA 79
 DB 310 TATGACACAGGTTTAAACA 328
 DB
 RESULT 8
 AAT49281
 ID AAT49281 standard; DNA; 1411 BP.
 AC AAT49281;
 XX
 DT 17-OCT-2003 (revised)
 DT 18-SEP-1997 (first entry)
 XX
 DE DNA encoding B. lactofermentum dihydrodipicolinate reductase.
 XX
 KW Corynebacterium, aspartokinase; feedback inhibition; L-lysine;
 KW L-threonine; dihydrodipicolinate; reductase; synthase; synthetase;
 KW diaminopimelate; decarboxylase; dehydrogenase; recombinant; production;
 KW manufacture; fermentation; corynebacteria; ds.
 XX
 OS Corynebacterium glutamicum.
 XX
 FH Key Location/Qualifiers
 FT CDS 311..1216
 FT /*tag= a
 FT /product= "dihydrodipicolinate_reductase"
 XX
 PN W09640934-A1.
 XX
 PD 19-DEC-1996.
 XX
 PF 05-JUN-1996; 96MO-JP001511.
 XX
 PR 07-JUN-1995; 95JP-00140614.
 XX
 PA (AJIN) AJINOMOTO CO INC.
 PI Otsuna S, Sugimoto M, Izui M, Hayakawa A, Nakano E, Kobayashi M;

PI Yoshihara Y, Nakamatsu T;
 XX
 DR WPI; 1997-052331/05.
 DR P-PSDB; AAW06582.
 XX
 PT L-lysine production by culture of transformed Corynebacterium - using DNA
 PT encoding aspartokinase lacking feedback inhibition by L-lysine, with DNA
 PT coding for dihydrodipicolinate reductase.
 XX
 PS Example 3; Page 48-51; 90pp; Japanese.
 XX
 CC A novel recombinant DNA sequence functional in Corynebacterium, comprises
 CC a DNA sequence encoding an aspartokinase, in which feedback inhibition by
 CC L-lysine and L-threonine has been reduced, and a DNA sequence encoding
 CC dihydrodipicolinate reductase and/or synthase, and/or diaminopimelate
 CC decarboxylase and/or dehydrogenase, e.g. the present Brevibacterium
 CC lactofermentum (ATCC 13669) dihydrodipicolinate reductase DNA sequence. A
 CC Corynebacterium host transformed with the recombinant DNA sequence may be
 CC used in the manufacture of L-lysine by fermentation, with an improved
 CC yield and a lower fall off of production rate with culture time. (Updated
 CC on 17-OCT-2003 to standardise OS field)
 CC
 SQ Sequence 1411 BP; 360 A; 343 C; 374 G; 334 T; 0 U; 0 Other;
 XX
 Query Match 98.0%; Score 77.4; DB 2; Length 1411;
 Best Local Similarity 98.7%; Pred. No. 1e-18; 1; Indels 0; Gaps 0;
 Matches 78; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GTTAGGTTTTTTCGGGGGTTGTTTAAACCCCAATGAGGAGAGTGAACCTTGAATC 60
 DB 250 GTTAGGTTTTTTCGGGGGTTGTTTAAACCCCAATGAGGAGAGTGAACCTTGAATC 309
 QY 61 TATGACACAGGTTTAAACA 79
 DB 310 TATGACACAGGTTTAAACA 328
 DB
 RESULT 9
 AAV40256
 ID AAV40256 standard; DNA; 1411 BP.
 AC AAV40256;
 XX
 DT 17-OCT-2003 (revised)
 DT 13-OCT-1998 (first entry)
 XX
 DE Brevibacterium lactofermentum dapA gene.
 XX
 KW Brevibacterium lactofermentum; lysC; L-lysine; coryneform bacterium;
 KW aspartokinase; feedback inhibition; dihydrodipicolinate reductase;
 KW diaminopimelate decarboxylase; aspartate aminotransferase; ds.
 XX
 OS Corynebacterium glutamicum.
 XX
 FH Key Location/Qualifiers
 FT CDS 311..1213
 FT /*tag= a
 FT /product= "dapA"
 XX
 PN EP854189-A2.
 XX
 PD 22-JUL-1998.
 XX
 PF 05-DEC-1997; 97EP-00121443.
 XX
 PR 05-DEC-1996; 96JP-00325659.
 XX
 PA (AJIN) AJINOMOTO CO INC.
 PI Arai M, Sugimoto M, Yoshihara Y, Nakamatsu T;
 XX
 DR WPI; 1998-379060/33.
 DR P-PSDB; AAW69549.

```
XX Recombinant DNA autonomously replicable in coryneform bacteria - used to
PT produce L-lysine, codes for e.g. aspartokinase, di:hydroipicolinate
PT reductase and synthase and di:amino-pimelate decarboxylase.
XX
PS Example 3, Page 28-29; 59pp; English.
XX
CC The present invention describes a recombinant DNA autonomously replicable
CC in cells of coryneform bacteria (CB), comprising a DNA sequence coding
CC for an aspartokinase (AK) in which feedback inhibition by L-lysine and L-
CC threonine is desensitized, a DNA sequence coding for a
CC dihydroipicolinate reductase (DHPRI), a DNA sequence coding for
CC dihydroipicolinate synthase (DHPS), a DNA sequence coding for
CC diaminopimelate decarboxylase (DAMD) and a DNA sequence encoding dapA from
CC Brevibacterium lactofermentum. The present sequence encodes dapA from
CC Brevibacterium lactofermentum. The DNA and related products from the
CC present invention, can be used for improving L-lysine productivity by CB.
CC The L-lysine produced can be used as a fodder additive. (Updated on 17-
CC OCT-2003 to standardise OS field)
XX
SQ Sequence 1411 BP; 360 A; 343 C; 374 G; 334 T; 0 U; 0 Other;
XX
Query Match 98.0%; Score 77.4; DB 2; Length 1411;
Best Local Similarity 98.7%; Pred. No. 1e-18; 1; Indels 0; Gaps 0;
Matches 78; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GTTAGGTTTTTTCGCGGGTTTAAACCCCAATAGAGGAGATGTTACCTTGAATC 60
DB 250 GTTAGGTTTTTTCGCGGGTTTAAACCCCAATAGAGGAGATGTTACCTTGAATC 309
QY 61 TATGAGCAGAGTTTAA 79
DB 310 TATGAGCAGAGTTTAA 328
XX
RESULT 10
AAV15785
ID AAV15785 standard; DNA; 1411 BP.
XX
AC AAV15785;
XX
DT 17-OCT-2003 (revised)
DT 05-JUN-1998 (first entry)
XX
DE B. lactofermentum dihydroipicolinate reductase DNA.
XX
KM Dihydroipicolinate reductase; ds.
XX
OS Corynebacterium glutamicum.
XX
FH Key Location/Qualifiers
FT CDS 311..1216
FT /*tag= a
FT /product= "dihydroipicolinate_reductase"
XX
XX
EN EPI1682-A2.
XX
PD 10-DEC-1997.
XX
PF 02-JUN-1997; 97EP-00108764.
XX
PR 05-JUN-1996; 96JP-00142812.
XX
PA (AJIN ) AJINOMOTO CO INC.
XX
PI Hitano S, Sugimoto M, Nakano E, Izui M, Hayakawa A, Yoshinara Y;
XX Nakamatsu T;
XX
XX WPI; 1998-020947/03.
DR P-PSDB; AAM47403.
XX
PT Vector containing di:amino-pimelate decarboxylase and di:amino-pimelate
PT dehydrogenase genes - used for lysine production by overexpression in
```

```
PT coryneform bacteria.
PS
XX Example 4; Page 41-43; 63pp; English.
XX
CC The present sequence encodes Brevibacterium lactofermentum
CC dihydroipicolinate reductase. (Updated on 17-OCT-2003 to standardise OS
CC field)
XX
SQ Sequence 1411 BP; 360 A; 343 C; 374 G; 334 T; 0 U; 0 Other;
XX
Query Match 98.0%; Score 77.4; DB 2; Length 1411;
Best Local Similarity 98.7%; Pred. No. 1e-18; 1; Indels 0; Gaps 0;
Matches 78; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GTTAGGTTTTTTCGCGGGTTTAAACCCCAATAGAGGAGATGTTACCTTGAATC 60
DB 250 GTTAGGTTTTTTCGCGGGTTTAAACCCCAATAGAGGAGATGTTACCTTGAATC 309
QY 61 TATGAGCAGAGTTTAA 79
DB 310 TATGAGCAGAGTTTAA 328
XX
RESULT 11
AAH68530/C
ID AAH68530 standard; DNA; 349980 BP.
XX
AC AAH68530;
XX
DT 26-SEP-2001 (first entry)
XX
DE C glutamicum coding sequence fragment SEQ ID NO: 7065.
XX
KM Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
XX organic acid synthesis; ds.
XX
OS Corynebacterium glutamicum.
XX
PN EPI108790-A2.
XX
PD 20-JUN-2001.
XX
PF 18-DEC-2000; 2000EP-00127688.
XX
PR 16-DEC-1999; 99JP-00377484.
PR 07-APR-2000; 2000JP-00159162.
PR 03-AUG-2000; 2000JP-00280988.
XX
XX (KYOW ) KYOWA HAKKO KOGYO KK.
XX
XX Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;
XX Tateishi N, Senoh A, Ikeda M, Ozaki A;
XX
XX WPI; 2001-376931/40.
XX
XX
PT Novel polynucleotides derived from Coryneform bacteria, for identifying
PT mutation point of a gene, measuring expression of a gene, analyzing
PT expression profile or pattern of a gene and identifying homologous gene.
XX
PS Disclosure; SEQ ID NO 7065; 246pp + Sequence Listing; English.
XX
XX The present invention provides a number of nucleotide and protein
XX sequences from the Coryneform bacterium Corynebacterium glutamicum. These
XX sequences are useful for identifying the mutation point of a gene derived from a
XX mutant of coryneform bacterium, measuring expression amount and analyzing
XX the expression profile or expression pattern of a gene derived from
XX Coryneform bacterium, and identifying a homologue of a gene derived from
XX Coryneform bacterium. Coryneform bacteria are useful for producing amino
XX acids, nucleic acids, vitamins, saccharides and organic acids;
XX particularly L-lysine. The present sequence is a nucleic acid described
XX in the exemplification of the invention. Note: The sequence data for this
XX patent did not form part of the printed specification, but was obtained
XX in electronic format directly from the European Patent Office
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XX Sequence 349980 BP; 86896 A; 98023 C; 80939 G; 84122 T; 0 U; 0 Other;
SQ
Query Match      98.0%; Score 77.4; DB 5; Length 349980;
Best Local Similarity 98.7%; Pred. No. 5.4e-18;
Matches 78; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GTTAGGTTTTTGGCGGGTGTGTTAAACCCCAATGAGGAAGATGTAACCTTGAATC 60
DB 280244 GTTAGGTTTTTGGCGGGTGTGTTAAACCCCAATGAGGAAGATGTAACCTTGAATC 280185
OY 61 TATGAGCACAGGTTTACA 79
DB 280184 TATGAGCACAGGTTTACA 280166

RESULT 12
AAF26008
ID AAF26008 standard; DNA; 80 BP.
XX
AC AAF26008;
XX
DT 20-APR-2001 (first entry)
XX
DE C. glutamicum dapA mutant MC20 promoter DNA fragment SEQ ID 6.
XX
KM lysE; L-lysine; lysine exporter-carrier; dapA; aspartate kinase; lysC;
KM dihydrodipicolinate synthase; pyc; pyruvate carboxylase; dapB; promoter;
KM dihydrodipicolinate reductase; fodder additive; ss.
XX
OS Corynebacterium glutamicum.
XX
PN EP1067192-A1.
XX
PD 10-JAN-2001.
XX
PF 06-JUL-2000; 2000EP-00114501.
XX
PR 07-JUL-1999; 99DE-01031317.
XX
PA (DEGS ) DEGUSSA-HUELS AG.
XX (KERJ ) FORSCHUNGSZENTRUM JUELICH GMBH.
XX
PI Moeckel B, Pfeifferle W, Kreutzer C, Hans S, Rieping M;
PI Eggeling L, Sahn H, Patek M;
XX
DR WPI; 2001-125731/14.
XX
PT Coryneform bacteria for high level production of lysine, useful as feed
PT additive, overexpresses the lysE and at least one other gene,
PT particularly dapA.
XX
PS Claim 4; Page 18; 25pp; German.
XX
XX This invention describes a novel L-lysine producing coryneform bacterium
XX (A) with an amplified lysE (lysine exporter-carrier) gene in which at
XX least one of the additional genes dapA (dihydrodipicolinate synthase), lysC
XX (aspartate kinase), pyc (pyruvate carboxylase) and/or dapB
XX (dihydrodipicolinate reductase) is amplified and preferably overexpressed.
XX L-lysine is used as a fodder additive for animals. Overexpression of the
XX additional genes improves lysine production compared with amplification
XX of lysE only. Corynebacterium glutamicum DSM 5715 transformed with
XX vectors that overexpress (i) dapA and (ii) both lysE and dapB produced
XX lysine hydrochloride at 15.4 g/l after 48 hr culture at 33plusoc. The
XX same strain that overexpressed lysE only produced 11.1 g/l

SQ Sequence 80 BP; 24 A; 11 C; 21 G; 24 T; 0 U; 0 Other;

Query Match      78.0%; Score 61.6; DB 4; Length 80;
Best Local Similarity 93.8%; Pred. No. 3.8e-13;
Matches 75; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

OY 1 GTTAGGTTTTTGGCGGGTGTGTTAAACCCCAATGAGGAAGATGTAACCTTGAATC 59
DB 60 CTATGAGCACAGGTTTACA 79
OY 61 TATGAGCACAGGTTTACA 79
DB 61 CTATGAGCACAGGTTTACA 80

RESULT 14

```

```

DB 1 GTTAGGTTTTTGGCGGGTGTGTTAAACCCCAATGAGGAAGATGTAATTTGAATC 60
OY 60 CTATGAGCACAGGTTTACA 79
DB 61 CTATGAGCACAGGTTTACA 80

RESULT 13
AAF26025
ID AAF26025 standard; DNA; 80 BP.
XX
AC AAF26025;
XX
DT 20-APR-2001 (first entry)
XX
DE C. glutamicum dapA MA16 mutant promoter fragment SEQ ID 6.
XX
KM lysE; L-lysine; pyc; pyruvate carboxylase; dapA; lysine exporter-carrier;
KM dihydrodipicolinate synthase; lysC; aspartate kinase; lysE; dapB;
KM dihydrodipicolinate reductase; fodder additive; ss.
XX
OS Corynebacterium glutamicum.
XX
PN EP1067193-A1.
XX
PD 10-JAN-2001.
XX
PF 06-JUL-2000; 2000EP-00114502.
XX
PR 07-JUL-1999; 99DE-01031314.
XX
PA (DEGS ) DEGUSSA-HUELS AG.
XX (KERJ ) FORSCHUNGSZENTRUM JUELICH.
XX
PI Kreutzer C, Moeckel B, Pfeifferle W, Eggeling L, Sahn H, Patek M;
XX
DR WPI; 2001-140055/15.
XX
PT Coryneform bacteria for high level production of lysine, useful as feed
PT additive, overexpresses the pyc and at least one other gene, e.g. dapA,
PT dapB or lysE.
XX
PS Claim 4; Page 21; 28pp; German.
XX
XX This invention describes a novel L-lysine producing coryneform bacterium
XX (A) with an amplified pyc (pyruvate carboxylase) gene in which at least
XX one of the additional genes dapA (dihydrodipicolinate synthase), lysC
XX (aspartate kinase), lysE (lysine exporter-carrier) and/or dapB
XX (dihydrodipicolinate reductase) is amplified and preferably overexpressed.
XX L-lysine is used as a fodder additive for animals. Overexpression of the
XX additional genes improves lysine production compared with amplification
XX of pyc only. Corynebacterium glutamicum DSM 5715 transformed with vectors
XX that overexpress dapA and all of pyc, lysE and dapB produced lysine
XX hydrochloride at 17.6 g/l after 72 hr culture at 33plusoc. The same
XX strain that overexpressed pyc only produced 11.3 g/l

SQ Sequence 80 BP; 24 A; 11 C; 21 G; 24 T; 0 U; 0 Other;

Query Match      78.0%; Score 61.6; DB 4; Length 80;
Best Local Similarity 93.8%; Pred. No. 3.8e-13;
Matches 75; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

OY 1 GTTAGGTTTTTGGCGGGTGTGTTAAACCCCAATGAGGAAGATGTAACCTTGAATC 59
DB 60 CTATGAGCACAGGTTTACA 79
OY 61 TATGAGCACAGGTTTACA 79
DB 61 CTATGAGCACAGGTTTACA 80

RESULT 14

```

```

AAH45371
ID   AAH45371 standard, DNA; 1333 BP.
AC   AAH45371;
XX
XX
DT   11-SEP-2001 (first entry)
DE   C. thermoaminogenes lysin biosynthetic enzyme dapA DNA.
XX
XX   Heat-resistant; lysin biosynthesis; enzyme; coryneform;
KM   aspartate-semialdehyde dehydrogenase; dapA; ds.
XX
OS   Corynebacterium thermoaminogenes.
PN   JP2001120270-A.
XX
XX   08-MAY-2001.
XX
XX   01-NOV-1999; 99JP-00311148.
XX
XX   01-NOV-1999; 99JP-00311148.
XX
XX   (AJIN ) AJINOMOTO KK.
XX
XX   WPI; 2001-364760/38.
XX
XX   P-PSDB; AAG64043.
XX
XX   A heat-resistant lysin biosynthetic system enzyme gene of a high
PT   temperature-resistant coryneform microbe.
XX
XX   Example 5; Page 12-13; 27pp; Japanese.
XX
XX   The invention relates to a gene from a high temperature-resistant
CC   coryneform microbe that encodes a heat-resistant lysin biosynthetic
CC   enzyme. The enzyme has aspartate-semialdehyde dehydrogenase activity and
CC   can be used for growing amino acid-producing microbes. The present
CC   sequence encodes an enzyme of the invention
XX
XX   Sequence 1333 BP; 277 A; 405 C; 397 G; 254 T; 0 U; 0 Other;
SQ
XX
Query Match          61.0%; Score 48.2; DB 4; Length 1333;
Best Local Similarity 81.2%; Pred. No. 1e-07;
Matches 56; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
QY      11 TTGCGGGGTTGTTTAAACCCCAATGAGGAGAGATGTTAACTTGAACCTATGAGCACA 70
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      248 TTACGGGGTTGTGTAACCCGACCTAAGAGAGAGATGTTAACTTGTCTCATGAGCACA 307
QY      71 GGTTTAACA 79
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      308 GGTTTAACA 316
XX
RESULT 15
AAF26001/c
ID   AAF26001 standard, DNA; 40 BP.
AC   AAF26001;
XX
XX
DT   20-APR-2001 (first entry)
DE   C. glutamicum dapA mutant MC20 PCR primer dap2.
XX
XX   lysE; L-lysine; lysine exporter-carrier; dapA; aspartate kinase; lysC;
KM   dihydrodipicolinate synthase; pyc; pyruvate carboxylase; dapB; PCR primer;
KM   dihydrodipicolinate reductase; fodder additive; ss.
XX
XX   Corynebacterium glutamicum.
XX
XX   EPI067192-A1.
XX
XX   10-JAN-2001.
XX

```

```

PF   06-JUL-2000; 2000EP-00114501.
XX
XX   07-JUL-1999; 99DE-01031317.
XX
XX   (DEGS ) DEGUSA-HUELS AG.
XX
XX   (KERJ ) FORSCHUNGSZENTRUM JUELICH GMBH.
XX
XX   Moeckel B, Pfeifferle W, Kreutzer C, Hans S, Rieping M;
PI   Eggeling L, Sahm H, Patek M;
XX
XX   WPI; 2001-125731/14.
XX
XX   Coryneform bacteria for high level production of lysine, useful as feed
PT   additive, overexpresses the lysE and at least one other gene,
XX   particularly dapA.
XX
XX   Example 11; Page 11; 25pp; German.
XX
XX   This invention describes a novel L-lysine producing coryneform bacterium
CC   (A) with an amplified lysE (lysine exporter-carrier) gene in which at
CC   least one of the additional genes dapA (dihydrodipicolinate synthase), lysC
CC   (aspartate kinase), pyc (pyruvate carboxylase) and/or dapB
CC   (dihydrodipicolinate reductase) is amplified and preferably overexpressed.
CC   L-lysine is used as a fodder additive for animals. Overexpression of the
CC   additional genes improves lysine production compared with amplification
CC   of lysE only. Corynebacterium glutamicum DSM 5715 transformed with
CC   vectors that overexpress (i) dapA and (ii) both lysE and dapB produced
CC   lysine hydrochloride at 15.4 g/l after 48 hr culture at 33plusoc. The
CC   same strain that overexpressed lysE only produced 11.1 g/l
XX
XX   Sequence 40 BP; 8 A; 10 C; 8 G; 14 T; 0 U; 0 Other;
SQ
XX
Query Match          50.6%; Score 40; DB 4; Length 40;
Best Local Similarity 100.0%; Pred. No. 4.2e-05;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      30 CCAATGAGGAGAGATGTTAACTTGAACCTATGAGCAC 69
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      40 CCAATGAGGAGAGATGTTAACTTGAACCTATGAGCAC 1
XX
Search completed: July 13, 2005, 17:01:40
Job time : 68.0069 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using SW model

Run on: July 13, 2005, 17:00:03 ; Search time 489.728 Seconds
(without alignments)
6140.305 Million cell updates/sec

Title: US-10-804-120-5

Sequence: 1 gctaggtttctgcgggggtc.....ctatggcacaggtttaca 79

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : EST:
1: gb_est1:
2: gb_est2:
3: gb_hic:
4: gb_est3:
5: gb_est4:
6: gb_est5:
7: gb_est6:
8: gb_gsa1:
9: gb_gsa2:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	31.2	39.5	265	1	AA728069 LmbV39P7/
2	29.8	37.7	815	9	CR823956 GR0AA54C
3	29.8	37.7	818	9	CC520829 CH240.368
4	29.8	37.7	843	9	CR824024 GR0AA54C
5	29	36.7	979	5	BQ675212 AGENCOURT
6	28.6	36.2	499	7	CO670296 DG33-5812
7	28.6	36.2	624	4	BJ345906 BJ345906
8	28.6	36.2	665	4	BJ430191 BJ430191
9	28.6	36.2	674	7	CO588301 DG2-20b16
10	28.6	36.2	689	4	BU431542 BU431542
11	28.6	36.2	704	4	BU430317 BU430317
12	28.2	35.7	320	1	AU301906 AU301906
13	28.2	35.7	665	8	AZ640483 1M0502G03
14	28.2	35.7	1140	8	CC243055 CH261-84A
15	28	35.4	440	7	CO126481 GR_BD101
16	28	35.4	565	6	CB608752 AMGNNUC:N
17	28	35.4	653	5	BQ154700 NF095F071
18	28	35.4	889	7	CV266577 WSO203.B2
19	28	35.4	1007	9	AL066754 Drosophila
20	27.8	35.2	472	1	AA664084 ac04b06.8
21	27.8	35.2	754	1	AI124469 SMOVJ3CAN
22	27.8	35.2	784	9	EX183886 Dario rer
23	27.8	35.2	794	9	EX199920 Dario rer
24	27.6	34.9	660	4	BJ342553 BJ342553

25	27.6	34.9	687	9	BX214579 Dario rer
26	27.4	34.7	396	1	AV767878 AV767878
27	27.4	34.7	505	2	BE436731 EST407849
28	27.4	34.7	752	8	BZ039047 1ka22d02
29	27.2	34.4	418	7	CK105601 UA23PD09
30	27.2	34.4	716	9	CL764630 OR_BBA013
31	27.2	34.4	761	5	BU301411 603783931
32	27.2	34.4	820	5	BX467747 BX467747
33	27.2	34.4	841	5	BU525063 AGENCOURT
34	27.2	34.4	915	9	CG951244 MBEID3OTR
35	27.2	34.4	1101	9	AL072117 Drosophila
36	27.2	34.4	1159	9	AG075559 Pan trogl
37	27	34.2	387	7	CV461920 Lr_VJ2CF
38	27	34.2	446	7	CV461809 Lr_VJ2CF
39	27	34.2	748	9	AG134983 Pan trogl
40	27	34.2	919	7	CK259406 EST705484
41	27	34.2	919	7	CK274793 EST720871
42	27	34.2	921	7	CK259405 EST705483
43	27	34.2	946	7	CK277974 EST724052
44	26.8	33.9	301	2	BX389802 BX389802
45	26.8	33.9	509	2	BF602997 BF602997

ALIGNMENTS

RESULT 1
LOCUS AA728069/c
DEFINITION LmbV39P7/129M Leishmania major promastigote full length cDNA clone
129M 5', mRNA sequence.

ACCESSION AA728069
VERSION AA728069.1 GI:3926100
KEYWORDS EST.
SOURCE Leishmania major
ORGANISM Leishmania major
Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;
Leishmania.

REFERENCE
1 (bases 1 to 265)
Almeida, R., Sampato, I., Schneider, H. and Blackwell, J.M.
Analysis of Leishmania major promastigote library from different
stages of development
Unpublished (1998)

JOURNAL
On Jan 5, 1998 this sequence version replaced gi:2747026.

COMMENT
Contact: Blackwell JM
Cambridge Institute for Medical Research
Wellcome Trust/MRC Building, Addenbrooke's Hospital, Hills Road,
Cambridge CB2 2XY, UK
Tel: 01223 336 143
Fax: 01223 331 206
Email: jmb37@cus.cam.ac.uk

PCR Primers
The EST is 265bp in length
PCR Primers
FORWARD: GGAACAGCATGACCATG
BACKWARD: GGAACAGCATGACCATG
Seq primer: AATTAACCTCACTAAAGG
High quality sequence stop: 265.
Location/Qualifiers
1..265
/organism="Leishmania major"
/mol_type="mRNA"
/strain="LV39"
/db_xref="taxon:5664"
/clone="129M"
/cell_type="Promastigote"
/clone_1b="Leishmania major promastigote full length cDNA
library from logarithmic stage (day 7)"
/note="Vector: Lambda zap II; Site_1: XhoI; Site_2: NotI"

FEATURES

source

ORIGIN

Query Match 39.5%; Score 31.2; DB 1; Length 265;
Best Local Similarity 66.2%; Pred. No. 5.4;

Matches 45; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

Qy 4 AGGTTTTCGGGGGTTTAAACCCCAATGAGGAGATGCTTAACCTGATCTAT 63
 Db 152 AGGCTTTTGGGGGTTGTAATCGGCCCAAGCTCGGCAAGTGCACAGTAACAGCTCC 93

Qy 64 GAGCAGCAG 71
 Db 92 CAGCAGCAG 85

RESULT 2

CR823956/c

LOCUS CR823956 815 bp DNA linear GSS 27-SEP-2004
 DEFINITION GR00AA54CB05FMI INRA BAC Bos taurus genomic clone INRA_984E06, DNA

ACCESSION CR823956
 VERSION CR823956.1 GI:52760044

KEYWORDS GSS.
 SOURCE Bos taurus (cow)

ORGANISM

Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovinae; Bos

REFERENCE 1 (bases 1 to 815)

AUTHORS Eggen,A., Schibler,L. and Roy,A.
 TITLE Bovine BAC End Sequences from the INRA bovine BAC library

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 815)

AUTHORS Genoscope.
 TITLE Direct Submission
 JOURNAL Submitted (20-SEP-2004) Genoscope - Centre National de Sequencage :
 BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)

COMMENT - Web : www.genoscope.cns.fr

CONTACT: Andre Eggen
 Department of Animal Genetics - LGBC

INRA

78350 Jouy-en-Josas, France

Tel: 33 1 34 65 24 24

Fax: 33 1 34 65 24 78

Email: eggen@jouy.inra.fr

Clones are derived from the INRA bovine BAC library
 (http://locus.jouy.inra.fr/fpc/cattle_bac_map.htm). For BAC library
 availability, please contact Andre Eggen (eggen@jouy.inra.fr). This
 work was undertaken as part of the International Bovine BAC
 Mapping Consortium (IBBMC) by INRA (Jouy-en-Josas) and Genoscope
 (Evry) Plate: 984 row: E column: 06
 Seq primer: M13 Forward
 Class: BAC ends

FEATURES

source

Location/Qualifiers

1..815

/organism="Bos taurus"

/mol_type="genomic DNA"

/strain="bred: Holstein"

/db_xref="taxon:9913"

/clone="INRA_984E06"

/sex="Male"

/cell_type="fibroblast"

/clone_lib="INRA bovine BAC"

/note="Vector: pBlotBAC11, Site_1: HindIII; Holstein bull;
 INRA Bovine BAC library (Male) produced by Andre
 Eggen-genoscope sequence ID : GR00AA54CB05FMI"

ORIGIN

Query Match 37.7%; Score 29.8; DB 9; Length 815;

Best Local Similarity 75.5%; Pred. No. 20;

Matches 37; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 2 TTAGGTTTTCGGGGGTTTAAACCCCAATGAGGAGATGCTTA 50
 Db 728 TCAAGGTTTTCGGGGGTTTTCCTCTCTAAGGAGAGATGCTTA 680

RESULT 3

CC520829/c

LOCUS

DEFINITION CC520829 818 bp DNA linear GSS 17-JUN-2003
 CH240_36814.T7 CHORI-240 Bos taurus genomic clone CH240_36814,
 genomic survey sequence.

ACCESSION CC520829

VERSION CC520829.1 GI:31839117

KEYWORDS GSS.

SOURCE Bos taurus (cow)

ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovinae; Bos

REFERENCE 1 (bases 1 to 818)

AUTHORS Holt,R., Stott,J., Yang,G., Barber,S., Smailus,D., Prabhur,A.-L.,
 Tsai,M., Cloutier,A., Lee,D., Gilm,N., Olson,T., Mayo,M.,
 Butlerfield,Y., Kirkpatrick,R., Liu,J., Guin,R., Chan,A., Chiu,R.,
 Mathewson,C., Wye,N., Masson,A., Brown-John,M., Jones,S.,
 Schein,J., Marra,M., de Jong,P., McWilliam,S., Barris,W.,
 Dalrymple,B.P. and Tellam,R.
 TITLE Bovine BAC End Sequences from Library CHORI-240, PLATES 294 to 398
 JOURNAL Unpublished (2003)
 COMMENT Other GSSs: CH240_36814.TARBACT3P2
 Contact: Rob Holt

Sequencing
 The British Columbia Cancer Agency Genome Science Centre
 600 W. 10th Ave, Vancouver, British Columbia, Canada V5Z 4E6
 Tel: 604-877-6085
 Fax: 604-877-6276
 Email: rholt@bccgsc.ca

Clones are derived from the bovine BAC library CHORI-240
 (http://www.chori.org/bacpac/bovine240.htm). For BAC library
 availability, please contact Pieter de Jong (pdejong@mail.choi.org).
 Clones may be purchased from BACPAC Resources
 (http://www.chori.org/bacpac/ordering/information.htm). This work
 was undertaken as part of the International Bovine BAC Mapping
 Consortium (IBBMC) by CSIRO Livestock Industries, Australia and the
 British Columbia Genome Sciences Centre, Canada.
 Plate: 368 row: I column: 4
 Seq primer: T7
 Class: BAC ends.

FEATURES

source

Location/Qualifiers

1..818

/organism="Bos taurus"

/mol_type="genomic DNA"

/strain="bred: Hereford"

/db_xref="taxon:9913"

/clone="CH240_36814"

/sex="Male"

/cell_type="Blood"

/clone_lib="CHORI-240"

/note="Vector: pTARBACT.3, Site_1: MboI; Site_2: MboI;
 Hereford bull Ii Domino 99375; CHORI-240 Bovine BAC
 library (Male) produced by Pieter de Jong"

ORIGIN

Query Match 37.7%; Score 29.8; DB 9; Length 818;

Best Local Similarity 75.5%; Pred. No. 20;

Matches 37; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 2 TTAGGTTTTCGGGGGTTTAAACCCCAATGAGGAGATGCTTA 50
 Db 314 TCAAGGTTTTCGGGGGTTTTCCTCTCTAAGGAGAGATGCTTA 266

RESULT 4

CR824024/c

LOCUS

DEFINITION CR824024 843 bp DNA linear GSS 27-SEP-2004
 GR00AA54CB07FMI INRA BAC Bos taurus genomic clone INRA_982H08, DNA
 sequence, genomic survey sequence.

ACCESSION CR824024

VERSION CR824024.1 GI:52760112

KEYWORDS GSS.

SOURCE
ORGANISM Bos taurus (cow)
 Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
 1 (bases 1 to 843)
REFERENCE Eggen, A., Schibler, L. and Roy, A.
TITLE Bovine BAC End Sequences from the INRA bovine BAC library
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 843)
GENOSCOPE Genoscope.
DIRECT SUBMISSION Submitted (20-SEP-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr
URL - Web : www.genoscope.cns.fr)
CONTACT Andre Eggen
DEPARTMENT Department of Animal Genetics - LGBC
INRA INRA
 78350 Jouy-en-Josas, France
 Tel : 33 1 34 65 24 24
 Fax : 33 1 34 65 24 78
 Email : eggen@jouy.inra.fr
 Clones are derived from the INRA bovine BAC library (http://locus.jouy.inra.fr/fpc/cattle_bac_map.htm). For BAC library availability, please contact Andre Eggen (eggen@jouy.inra.fr). This work was undertaken as part of the International Bovine BAC Mapping Consortium (IBBMC) by INRA (Jouy-en-Josas) and Genoscope (Evry) Plate: 982 row: H column: 08
 Seq primer: M13 Forward
 Class: BAC ends.
FEATURES
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 /mol_type="genomic DNA"
 /strain="bred: Holstein"
 /db_xref="taxon:9913"
 /clone="INRA_982H08"
 /sex="Male"
 /cell_type="fibroblast"
 /clone_lib="INRA bovine BAC"
 /note="Vector: pBelBAC11; Site 1: HindIII; Holstein bull; INRA Bovine BAC library (Male) produced by Andre Eggen-Genoscope sequence ID : GR0AAS4CE07FM1"

ORIGIN
 Query Match 37.7%; Score 29.8; DB 9; Length 843;
 Best Local Similarity 75.5%; Pred. No. 20;
 Matches 37; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 2 TTAGGTTTTCGGGGGTTTAAACCCCAATGAGGAGATGATA 50
 |||||
 Db 729 TCAGGGTTTTCGGGGGTTTTCCTCTCTAAGGAGAGGTTGA 681

RESULT 5
LOCUS B0675212 979 bp mRNA linear EST 15-JUL-2002
DEFINITION AGENCOURT_8355129 NIH_MGC_102 Homo sapiens cDNA clone IMAGE:6275416
 5', mRNA sequence.
ACCESSION B0675212
VERSION B0675212.1 GI:21786046
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 979)
REFERENCE NIH-MGC http://mgc.nci.nih.gov/
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Straubeberg, Ph.D.
 Email: c9apbs-remail.nih.gov
 Tissue Procurement: ATCC

FEATURES
 source
 1..979
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6275416"
 /tissue_type="epidermoid carcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_102"
 /note="Organ: salivary gland; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN
 Query Match 36.7%; Score 29; DB 5; Length 979;
 Best Local Similarity 67.2%; Pred. No. 39;
 Matches 41; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 2 TTAGGTTTTCGGGGGTTTAAACCCCAATGAGGAGATGATACTTGA 61
 |||||
 Db 780 TTGGTTTTCGGGGGTTTTCCTCTCTAAGGAGAGGTTGA 839

QY 62 A 62
 |
 Db 840 A 840

RESULT 6
LOCUS CO670296/c 499 bp mRNA linear EST 26-JUL-2004
DEFINITION DG33-58j2 DG33-aorta Canis familiaris cDNA 3', mRNA sequence.
ACCESSION CO670296
VERSION CO670296.1 GI:50613981
KEYWORDS EST.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 1 (bases 1 to 499)
REFERENCE Schlueter, T., Hermanns, J., Weindel, M., Schnette, D., Kranz, H.,
 Henrich, J. and Loebbert, R.
AUTHORS Dog arrayTAG cDNA clone collection
JOURNAL Unpublished (2004)
COMMENT Contact: Thomas Schlueter
 LION Bioscience AG
 Walchoferstrasse 98, D-69123 Heidelberg, Germany
 Tel: +49 6221 4038 150
 Fax: +49 6221 4038 290
 Email: Thomas.Schlueter@lionbioscience.com.
FEATURES
 source
 1..499
 Location/Qualifiers
 /organism="Canis familiaris"
 /mol_type="mRNA"
 /strain="Beagle"
 /db_xref="taxon:9615"
 /tissue_type="aorta"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="DG33-aorta"

ORIGIN /note="Organ: aorta; Vector: Dog pBluescript LION"

Query Match 36.2%; Score 28.6; DB 7; Length 499;
 Best Local Similarity 64.2%; Pred. No. 48;
 Matches 43; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

Qy 13 GCGGGGTTGTTAAACCCCAATGAGGAGATGTAACCTTGACTCTATGACACAG 72
 Db 489 GTGGTTCCGTTGAGCTAAATAATGAGGTACATGTTGTAATCTTTGCTATCAT 430

Qy 73 TTAAACA 79
 Db 429 GTTAACA 423

RESULT 7
 B345906 624 bp mRNA linear EST 06-MAR-2002
 LOCUS B345906 Dictyostelium discoideum cDNA library, AF Dictyostelium
 DEFINITION B345906 Dictyostelium discoideum cDNA library, AF Dictyostelium
 ACCESSION B345906
 VERSION B345906.1 GI:19216413
 KEYWORDS EST.
 SOURCE Dictyostelium discoideum
 ORGANISM Dictyostelium discoideum
 Eukaryota; Mycetozoa; Dictyostellida; Dictyostellium.
 REFERENCE 1 (bases 1 to 624)
 AUTHORS Urushihara, H., Tanaka, Y., Kohara, Y., and Shin-i, T.
 TITLE Full length cDNA of Dictyostelium discoideum at the aggregation stage
 JOURNAL Unpublished (2002)
 COMMENT Contact: Tadasu Shin-i
 Center For Genetic Resource Information
 National Institute of Genetics
 1111 Yata, Mishima, Shizuoka 411-8540, Japan
 Tel: 81-559-81-6856
 Fax: 81-559-81-6855
 Email: tshini@genes.nig.ac.jp.
 Location/Qualifiers
 FEATURES
 source 1..624
 /organism="Dictyostelium discoideum"
 /mol_type="mRNA"
 /strain="AX4"
 /db_xref="taxon:44689"
 /clone="dd429p09"
 /sex="mat A"
 /dev_stage="Aggregation stage"
 /clone_lib="Dictyostelium discoideum cDNA library, AF"

ORIGIN

Query Match 36.2%; Score 28.6; DB 4; Length 624;
 Best Local Similarity 72.5%; Pred. No. 49;
 Matches 37; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 18 GTTGTTAACCCCAATGAGGAGATGTAACCTTGACTCTATGACGA 68
 Db 530 GTGGTTAAATCAACCAATGATGATATGGAACCATGTACACTTTAGCA 580

RESULT 8
 B3430191 665 bp mRNA linear EST 13-MAR-2002
 LOCUS B3430191 Dictyostelium discoideum cDNA library, VF Dictyostelium
 DEFINITION B3430191 Dictyostelium discoideum cDNA library, VF Dictyostelium
 ACCESSION B3430191 GI:19404913
 VERSION B3430191.1
 KEYWORDS EST.
 SOURCE Dictyostelium discoideum
 ORGANISM Dictyostelium discoideum
 Eukaryota; Mycetozoa; Dictyostellida; Dictyostellium.
 REFERENCE 1 (bases 1 to 665)
 AUTHORS Urushihara, H., Tanaka, Y., Kohara, Y., and Shin-i, T.

TITLE Full length cDNA of Dictyostelium discoideum at the vegetative stage
 JOURNAL Unpublished (2002)
 COMMENT Contact: Tadasu Shin-i
 Center For Genetic Resource Information
 National Institute of Genetics
 1111 Yata, Mishima, Shizuoka 411-8540, Japan
 Tel: 81-559-81-6856
 Fax: 81-559-81-6855
 Email: tshini@genes.nig.ac.jp.
 Location/Qualifiers
 FEATURES
 source 1..665
 /organism="Dictyostelium discoideum"
 /mol_type="mRNA"
 /strain="AX4"
 /db_xref="taxon:44689"
 /clone="ddv6108"
 /sex="mat A"
 /dev_stage="Growth phase"
 /clone_lib="Dictyostelium discoideum cDNA library, VF"

ORIGIN

Query Match 36.2%; Score 28.6; DB 4; Length 665;
 Best Local Similarity 72.5%; Pred. No. 50;
 Matches 37; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 18 GTTGTTAACCCCAATGAGGAGATGTAACCTTGACTCTATGACGA 68
 Db 571 GTGGTTAAATCAACCAATGATGATATGGAACCATGTACACTTTAGCA 621

RESULT 9
 C0588301 674 bp mRNA linear EST 21-JUL-2004
 LOCUS C0588301 DG2-20b16 Canis familiaris cDNA 3', mRNA sequence.
 DEFINITION DG2-20b16 Canis familiaris cDNA 3', mRNA sequence.
 ACCESSION C0588301
 VERSION C0588301.1 GI:50433822
 KEYWORDS EST.
 SOURCE Canis familiaris (dog)
 ORGANISM Canis familiaris
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 REFERENCE 1 (bases 1 to 674)
 AUTHORS Schlueter, T., Hermanns, J., Weindel, M., Schuette, D., Kranz, H.,
 Henrich, J., and Loebbert, R.
 TITLE Dog arrayTAG cDNA clone collection
 JOURNAL Unpublished (2004)
 COMMENT Contact: Thomas Schlueter
 LION bioscience AG
 Walhoferstrasse 98, D-69123 Heidelberg, Germany
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 Fax: +49 6221 4038 290
 Email: Thomas.Schlueter@lionbioscience.com.
 Location/Qualifiers
 FEATURES
 source 1..674
 /organism="Canis familiaris"
 /mol_type="mRNA"
 /strain="Beagle"
 /db_xref="taxon:9615"
 /tissue_type="brain"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="DG2-brain"
 /note="Organ: brain; Vector: Dog pBluescript LION"

ORIGIN

Query Match 36.2%; Score 28.6; DB 7; Length 674;
 Best Local Similarity 64.2%; Pred. No. 50;
 Matches 43; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

Qy 13 GCGGGGTTGTTAAACCCCAATGAGGAGATGTAACCTTGACTCTATGACACAG 72
 Db 486 GTGGTTCCGTTGAGCTAAATAATGAGGTACATGTTGTAATCTTTGCTATCAT 427

Qy 73 TTAAACA 79
 Db 426 GTTAACA 420

RESULT 10
 BJA31542 689 bp mRNA linear EST 13-MAR-2002
 LOCUS BJA31542
 DEFINITION Dictyostelium discoideum cDNA library, VF Dictyostelium
 accession cDNA clone d4v14e16 3', mRNA sequence.

ACCESSION BJA31542
 VERSION BJA31542.1 GI:19406264
 KEYWORDS EST.
 SOURCE Dictyostelium discoideum
 ORGANISM Dictyostelium discoideum
 Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
 1 (bases 1 to 689)
 Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-I,T.
 Full length cDNA of Dictyostelium discoideum at the vegetative
 stage

JOURNAL
 COMMENT Unpublished (2002)
 Contact: Tadao Shin-i
 Center For Genetic Resource Information
 National Institute of Genetics
 1111 Yata, Mishima, Shizuoka 411-8540, Japan
 Tel: 81-559-81-6856
 Fax: 81-559-81-6855
 Email: tshini@genes.nig.ac.jp.
 Location/Qualifiers
 1..689
 /organism="Dictyostelium discoideum"
 /mol_type="mRNA"
 /strain="AX4"
 /db_xref="taxon:44689"
 /clone="d4v14e16"
 /sex="mat A"
 /dev_stage="Growth phase"
 /clone_1fb="Dictyostelium discoideum cDNA library, VF"

ORIGIN
 Query Match 36.2%; Score 28.6; DB 4; Length 689;
 Best Local Similarity 72.5%; Pred. No. 50;
 Matches 37; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 18 GTTGTAAACCCCAATGAGGAGATGTAACCTTGAACTATAGACA 68
 Db 497 GTGGTTAAATCACCACCAATGCATGATATGGAACCAATGACACTTTTACCA 547

RESULT 11
 BJA30317 704 bp mRNA linear EST 13-MAR-2002
 LOCUS BJA30317
 DEFINITION Dictyostelium discoideum cDNA library, VF Dictyostelium
 accession cDNA clone d4v6g22 3', mRNA sequence.

ACCESSION BJA30317
 VERSION BJA30317.1 GI:19405039
 KEYWORDS EST.
 SOURCE Dictyostelium discoideum
 ORGANISM Dictyostelium discoideum
 Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
 1 (bases 1 to 704)
 Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-I,T.
 Full length cDNA of Dictyostelium discoideum at the vegetative
 stage

JOURNAL
 COMMENT Unpublished (2002)
 Contact: Tadao Shin-i
 Center For Genetic Resource Information
 National Institute of Genetics
 1111 Yata, Mishima, Shizuoka 411-8540, Japan
 Tel: 81-559-81-6856
 Fax: 81-559-81-6855
 Email: tshini@genes.nig.ac.jp.

FEATURES
 source Location/Qualifiers
 1..704
 /organism="Dictyostelium discoideum"
 /mol_type="mRNA"
 /strain="AX4"
 /db_xref="taxon:44689"
 /clone="d4v6g22"
 /sex="mat A"
 /dev_stage="Growth phase"
 /clone_1fb="Dictyostelium discoideum cDNA library, VF"

ORIGIN
 Query Match 36.2%; Score 28.6; DB 4; Length 704;
 Best Local Similarity 72.5%; Pred. No. 50;
 Matches 37; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 18 GTTGTAAACCCCAATGAGGAGATGTAACCTTGAACTATAGACA 68
 Db 536 GTGGTTAAATCACCACCAATGCATGATATGGAACCAATGACACTTTTACCA 586

RESULT 12
 AU301906 320 bp mRNA linear EST 22-JAN-2004
 LOCUS AU301906
 DEFINITION zinnia cultured mesophyll cell equalized cDNA zinnia
 elegans cDNA clone Z10294, mRNA sequence.

ACCESSION AU301906
 VERSION AU301906.1 GI:41117765
 KEYWORDS EST.
 SOURCE zinnia elegans
 ORGANISM zinnia elegans
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; campanulids; Asterales; Asteraceae; Asteroideae;
 Helianthaceae; Zinnia.
 1 (bases 1 to 320)
 Demura,T., Taahiro,G., Horiguchi,G., Kishimoto,N., Kubo,M.,
 Matsumoto,N., Minami,A., Nagata-Hiataishi,M., Nakamura,K.,
 Okamura,Y., Sassa,N., Suzuki,S., Yazaki,J., Kikuchi,S. and
 Fukuda,H.
 Visualization by comprehensive microarray analysis of gene
 expression programs during transdifferentiation of mesophyll cells
 into xylem cells
 Proc. Natl. Acad. Sci. U.S.A. 99 (24), 15794-15799 (2002)
 Contact: Taku Demura
 Morphogenesis Research Group
 RIKEN Plant Science Center
 1-7-22 Suehirocho, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9605
 Fax: 81-45-503-9573
 Email: demura@postman.riken.go.jp
 This clone was obtained at our laboratory
 Seq primer: M13 forward.
 Location/Qualifiers
 1..320
 /organism="zinnia elegans"
 /mol_type="mRNA"
 /cultivar="Canary bird"
 /db_xref="taxon:34245"
 /clone="Z10294"
 /issue_type="mesophyll cell"
 /clone_1fb="zinnia cultured mesophyll cell equalized cDNA"
 /note="Vector: pGEM-T easy; cultured in tracheary element
 differentiation-inductive medium"

ORIGIN
 Query Match 35.7%; Score 28.2; DB 1; Length 320;
 Best Local Similarity 68.4%; Pred. No. 61;
 Matches 39; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

Qy 2 TTAGGTTTTTTGGGGGTTGTTAAACCCCAATGAGGAGATGTAACCTTGAAAC 58
 Db 193 TTCATTTTCTTCGGGTTGTTAAATCCCAACGAGCAATATGACATATTATGAC 249

RESULT 13
 AZ640483/c 665 bp DNA linear GSS 14-DEC-2000
 LOCUS 1M0502G03R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 DEFINITION UUGC1M0502G03 R, genomic survey sequence.
 ACCESSION AZ640483
 VERSION AZ640483.1 GI:11763883
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murine; Mus.
 1 (bases 1 to 665)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausen, A. and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert length: 10000 Std Error: 0.00
 Plate: 0502 row: G column: 03
 Seg primer: CACACAGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 665.
 Location/Qualifiers
 1. 665
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0502G03"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PMD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 Kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PMD42 (g114732114[gb|AF129072.1]), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

ORIGIN
 Query Match 35.7%; Score 28.2; DB 8; Length 665;
 Best Local Similarity 68.4%; Pred. No. 69;
 Matches 39; Conservative 0; Mismatches 18; Indels 0; Gaps 0;
 2 TTAGGTTTTTGGGGGTTGTTTAAACCCCAATGAGGAGATGTACTTAAC 58
 393 TTAGTACTTTTCCAAATTTTCAAGCAGATGAGGCCGATTTAACTTTAAC 337

RESULT 14
 CC243055/c 1140 bp DNA linear GSS 12-MAY-2003
 LOCUS CH261-84A2 RML.1 CH261 Gallus gallus genomic clone CH261-84A2,
 DEFINITION genomic survey sequence.
 ACCESSION CC243055
 VERSION CC243055.1 GI:30569718
 KEYWORDS GSS.
 SOURCE Gallus gallus (chicken)
 ORGANISM Gallus gallus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianinae; Gallus.
 1 (bases 1 to 1140)
 Kremetzki, C., Higginbotham, J., Wylie, K., Carter, J., McPherson, J.,
 Warren, W., Graves, T., Mardis, E. and Wilson, R.
 Gallus gallus BAC End Reads
 JOURNAL Unpublished (2003)
 COMMENT Contact: Richard K. Wilson
 Genome Sequencing Center
 Washington University School of Medicine
 Email: submissions@wustl.edu
 Insert length: 18200 Std Error: 0.00
 Seq primer: RML TRACACTCTACTTATGAGACA
 Class: BAC ends
 High quality sequence start: 34
 High quality sequence stop: 581.
 Location/Qualifiers
 1. 1140
 /organism="Gallus gallus"
 /mol_type="genomic DNA"
 /strain="Red Jungle Fowl"
 /db_xref="taxon:9031"
 /clone="CH261-84A2"
 /sex="female"
 /cell_line="UCD001, inbred 256"
 /clone_lib="CH261"
 /note="Vector: PTARBAC2.1, site_1: EcoRI, site_2: EcoRI;
 CH261 Female Chicken library - for library and clone
 ordering information: http://www.choi.org/bacpac"

ORIGIN
 Query Match 35.7%; Score 28.2; DB 8; Length 1140;
 Best Local Similarity 63.6%; Pred. No. 75;
 Matches 42; Conservative 0; Mismatches 24; Indels 0; Gaps 0;
 5 GGTGTTTTGGGGGCTGTTTAAACCCCAATGAGGAGATGTACTTAAC 64
 1047 GGTGTTTTGGGGGCTGTTTAAACCCCAATGAGGAGATGTACTTAAC 988
 65 AGCACA 70
 987 GCGACA 982

RESULT 15
 CO126481 440 bp mRNA linear EST 16-JUN-2004
 LOCUS GR_Eb01012.r GR_Eb Gossypium raimondii cDNA clone GR_Eb01012.3',
 DEFINITION mRNA sequence.
 ACCESSION CO126481
 VERSION CO126481.1 GI:48828091
 KEYWORDS EST.
 SOURCE Gossypium raimondii
 ORGANISM Gossypium raimondii
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eustosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
 1 (bases 1 to 440)
 Kim, H., Yu, Y., Kudrna, D., Hatfield, J., Stum, D., Mueller, C.,
 Udall, J. A., Rapp, R. A., Wendel, J. F., Rao, K., Soderlund, C. and

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